

SEQUENCE LISTING

(1) GENERAL INFORMATION:

(i) APPLICANT: JOHNSON, EUGENE M
MILBRANDT, JEFFREY D
KOTZBAUER, PAUL T
LAMPE, PATRICIA A
KLEIN, ROBERT
DESAUVAGE, FRED



(ii) TITLE OF INVENTION: PERSEPHIN AND RELATED GROWTH FACTOR

(iii) NUMBER OF SEQUENCES: 242

(iv) CORRESPONDENCE ADDRESS:

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(v) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: Floppy disk
(B) COMPUTER: IBM PC compatible
(C) OPERATING SYSTEM: PC-DOS/MS-DOS
(D) SOFTWARE: PatentIn Release #1.0, Version #1.30

(vi) CURRENT APPLICATION DATA:

(A) APPLICATION NUMBER: 09/220,617
(B) FILING DATE: 24 Dec. 1998
(C) CLASSIFICATION:

(viii) ATTORNEY/AGENT INFORMATION:

(A) NAME: GENDLOFF, ELIE H.
(B) REGISTRATION NUMBER: 44,704
(C) REFERENCE/DOCKET NUMBER: 6029-7976

(ix) TELECOMMUNICATION INFORMATION:

(A) TELEPHONE: 314-727-5188
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(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 102 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

Ala Arg Leu Gly Ala Arg Pro Cys Gly Leu Arg Glu Leu Glu Val Arg
1 5 10 15
Val Ser Glu Leu Gly Leu Gly Tyr Ala Ser Asp Glu Thr Val Leu Phe
20 25 30

Arg Tyr Cys Ala Gly Ala Cys Glu Ala Ala Ala Arg Val Tyr Asp Leu
 35 40 45

Gly Leu Arg Arg Leu Arg Gln Arg Arg Arg Leu Arg Arg Glu Arg Val
 50 55 60

Arg Ala Gln Pro Cys Cys Arg Pro Thr Ala Tyr Glu Asp Glu Val Ser
 65 70 75 80

Phe Leu Asp Ala His Ser Arg Tyr His Thr Val His Glu Leu Ser Ala
 85 90 95

Arg Glu Cys Ala Cys Val
 100

(2) INFORMATION FOR SEQ ID NO:2:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 100 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Pro Gly Ala Arg Pro Cys Gly Leu Arg Glu Leu Glu Val Arg Val Ser
 1 5 10 15

Glu Leu Gly Leu Gly Tyr Thr Ser Asp Glu Thr Val Leu Phe Arg Tyr
 20 25 30

Cys Ala Gly Ala Cys Glu Ala Ala Ile Arg Ile Tyr Asp Leu Gly Leu
 35 40 45

Arg Arg Leu Arg Gln Arg Arg Arg Val Arg Arg Glu Arg Ala Arg Ala
 50 55 60

His Pro Cys Cys Arg Pro Thr Ala Tyr Glu Asp Glu Val Ser Phe Leu
 65 70 75 80

Asp Val His Ser Arg Tyr His Thr Leu Gln Glu Leu Ser Ala Arg Glu
 85 90 95

Cys Ala Cys Val
 100

(2) INFORMATION FOR SEQ ID NO:3:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 16 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
 (B) LOCATION: 6
 (D) OTHER INFORMATION: /note= "ANY AMINO ACID"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

Ser Gly Ala Arg Pro Xaa Gly Leu Arg Glu Leu Glu Val Ser Val Ser
 1 5 10 15

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 10 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 1
- (D) OTHER INFORMATION: /note= "ANY AMINO ACID"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 6
- (D) OTHER INFORMATION: /note= "SERINE OR CYSTEINE"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

Xaa Cys Ala Gly Ala Xaa Glu Ala Ala Val
 1 5 10

(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 23 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 1
- (D) OTHER INFORMATION: /note= "ANY AMINO ACID"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 2
- (D) OTHER INFORMATION: /note= "ANY AMINO ACID"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 17
- (D) OTHER INFORMATION: /note= "GLUTAMINE OR GLUTAMIC ACID"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

Xaa Xaa Val Glu Ala Lys Pro Cys Cys Gly Pro Thr Ala Tyr Glu Asp
 1 5 10 15

Xaa Val Ser Phe Leu Ser Val
20

(2) INFORMATION FOR SEQ ID NO:6:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 10 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

Tyr His Thr Leu Gln Glu Leu Ser Ala Arg
1 5 10

(2) INFORMATION FOR SEQ ID NO:7:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 197 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

Met Gln Arg Trp Lys Ala Ala Ala Leu Ala Ser Val Leu Cys Ser Ser
1 5 10 15

Val Leu Ser Ile Trp Met Cys Arg Glu Gly Leu Leu Leu Ser His Arg
20 25 30

Leu Gly Pro Ala Leu Val Pro Leu His Arg Leu Pro Arg Thr Leu Asp
35 40 45

Ala Arg Ile Ala Arg Leu Ala Gln Tyr Arg Ala Leu Leu Gln Gly Ala
50 55 60

Pro Asp Ala Met Glu Leu Arg Glu Leu Thr Pro Trp Ala Gly Arg Pro
65 70 75 80

Pro Gly Pro Arg Arg Arg Ala Gly Pro Arg Arg Arg Arg Ala Arg Ala
85 90 95

Arg Leu Gly Ala Arg Pro Cys Gly Leu Arg Glu Leu Glu Val Arg Val
100 105 110

Ser Glu Leu Gly Leu Gly Tyr Ala Ser Asp Glu Thr Val Leu Phe Arg
115 120 125

Tyr Cys Ala Gly Ala Cys Glu Ala Ala Ala Arg Val Tyr Asp Leu Gly
130 135 140

Leu Arg Arg Leu Arg Gln Arg Arg Arg Leu Arg Arg Glu Arg Val Arg
145 150 155 160

Leu Asp Ala His Ser Arg Tyr His Thr Val His Glu Leu Ser Ala Arg
180 185 190

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 195 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

Leu Leu Ser Val Trp Met Cys Gln Glu Gly Leu Leu Leu Gly His Arg
20 25 30

Leu Gly Pro Ala Leu Ala Pro Leu Arg Arg Pro Pro Arg Thr Leu Asp
35 40 45

Ala Arg Ile Ala Arg Leu Ala Gln Tyr Arg Ala Leu Leu Gln Gly Ala
50 55 60

Pro Asp Ala Val Glu Leu Arg Glu Leu Ser Pro Trp Ala Ala Arg Ile
65 70 75 80

Pro Gly Pro Arg Arg Arg Ala Gly Pro Arg Arg Arg Arg Ala Arg Pro
85 90 95

Gly Ala Arg Pro Cys Gly Leu Arg Glu Leu Glu Val Arg Val Ser Glu
100 105 110

Leu Gly Leu Gly Tyr Thr Ser Asp Glu Thr Val Leu Phe Arg Tyr Cys
115 120 125

Ala Gly Ala Cys Glu Ala Ala Ile Arg Ile Tyr Asp Leu Gly Leu Arg
130 135 140

Arg Leu Arg Gln Arg Arg Arg Val Arg Arg Glu Arg Ala Arg Ala His
145 150 155 160

Pro Cys Cys Arg Pro Thr Ala Tyr Glu Asp Glu Val Ser Phe Leu Asp
165 170 175

Val His Ser Arg Tyr His Thr Leu Gln Glu Leu Ser Ala Arg Glu Cys
180 185 190

Ala Cys Val
195

(i). SEQUENCE CHARACTERISTICS:
(A) LENGTH: 306 base pairs

(B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

| | |
|---|-----|
| GCGCGGTTGG GGGCGCGGCC TTGCGGGCTG CGCGAGCTGG AGGTGCGCGT GAGCGAGCTG | 60 |
| GGCCTGGGCT ACGCGTCCGA CGAGACGGTG CTGTTCCGCT ACTGCGCAGG CGCCTGCGAG | 120 |
| GCTGCCGCGC GCGTCTACGA CCTCGGGCTG CGACGACTGC GCCAGCGGCG GCGCCTGCGG | 180 |
| CGGGAGCGGG TGC GCGCGCA GCCCTGCTGC CGCCGACGG CCTACGAGGA CGAGGTGTCC | 240 |
| TTCCTGGACG CGCACAGCCG CTACCACACG GTGCACGAGC TGTCGGCGCG CGAGTGCGCC | 300 |
| TGCGTG | 306 |

(2) INFORMATION FOR SEQ ID NO:10:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 300 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

| | |
|---|-----|
| CCGGGGGCTC GGCTTGTGG GCTGCGGAG CTCGAGGTGC GCGTGAGCGA GCTGGGCCTG | 60 |
| GGCTACACGT CGGATGAGAC CGTGCTGTTT CGTACTGCG CAGGCGCGTG CGAGGCGGCC | 120 |
| ATCCGCATCT ACGACCTGGG CCTTCGGCGC CTGCGCCAGC GGAGGCGCGT GCGCAGAGAG | 180 |
| CGGGCGCGGG CGCACCCGTG TTGTCGCCCC ACGGCCTATG AGGACGAGGT GTCCTTCCTG | 240 |
| GACGTGCACA GCCGCTACCA CACGCTGCAA GAGCTGTCGG CGCGGGAGTG CGCGTGCGTG | 300 |

(2) INFORMATION FOR SEQ ID NO:11:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 594 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

| | |
|---|-----|
| ATGCAGCGCT GGAAGGCGGC GGCCTTGGCC TCAGTGCTCT GCAGCTCCGT GCTGTCCATC | 60 |
| TGGATGTGTC GAGAGGGCCT GCTTCTCAGC CACCGCCTCG GACCTGCGCT GGTCCCCCTG | 120 |
| CACCGCCTGC CTCGAACCTT GGACGCCCCG ATTGCCCCGC TGGCCAGTA CCGTGCACTC | 180 |

CTGCAGGGGG CCCC GGATGC GATGGAGCTG CGCGAGCTGA CGCCCTGGGC TGGGCGGCCC 240
 CCAGGTCCGC GCCGTCGGGC GGGGCCCCGG CGGCGGCGCG CGCGTGCGCG GTTGGGGGCG 300
 CGGCCTTGCG GGCTGCGCGA GCTGGAGGTG CGCGTGAGCG AGCTGGGCCT GGGCTACGCG 360
 TCCGACGAGA CGGTGCTGTT CCGCTACTGC GCAGGCGCCT GCGAGGCTGC CGCGCGCGTC 420
 TACGACCTCG GGCTGCGACG ACTGCGCCAG CGGCGGCGCC TCGGCGGGA GCGGGTGCGC 480
 GCGCAGCCCT GCTGCCGCCC GACGGCCTAC GAGGACGAGG TGTCCTTCCT GGACGCGCAC 540
 AGCCGCTACC ACACGGTGCA CGAGCTGTCG GCGCGCGAGT GCGCCTGCGT GTGA 594

(2) INFORMATION FOR SEQ ID NO:12:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 588 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

ATGAGGCGCT GGAAGGCAGC GGCCCTGGTG TCGCTCATCT GCAGCTCCCT GCTATCTGTC 60
 TGGATGTGCC AGGAGGGTCT GCTCTTGGGC CACCGCCTGG GACCCGCGCT TGCCCCGCTA 120
 CGACGCCCTC CACGCACCCT GGACGCCCGC ATCGCCCGCC TGGCCAGTA TCGCGCTCTG 180
 CTCCAGGGCG CCCCCGACGC GGTGGAGCTT CGAGAAGTTT CTCCCTGGGC TGCCCGCATC 240
 CCGGGACCGC GCCGTCGAGC GGGTCCCCGG CGTCGGCGGG CGCGGCCGGG GGCTCGGCCT 300
 TGTGGGCTGC GCGAGCTCGA GGTGCGCGTG AGCGAGCTGG GCCTGGGCTA CACGTCGGAT 360
 GAGACCGTGC TGTTCGCTA CTGCGCAGGC GCGTGCGAGG CGGCCATCCG CATCTACGAC 420
 CTGGGCCCTT GCGGCCTGCG CCAGCGGAGG CGCGTGCGCA GAGAGCGGGC GCGGGCGCAC 480
 CCGTGTGTGC GCCCGACGGC CTATGAGGAC GAGGTGTCTT TCCTGGACGT GCACAGCCGC 540
 TACCACACGC TGCAAGAGCT GTCGGCGCGG GAGTGCGCGT GCGTGTGA 588

(2) INFORMATION FOR SEQ ID NO:13:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 348 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

GGAGGGAGAG CGGCGGTGG TTTCGTCCGT GTGCCCCGCG CCCGGCGCTC CTCGCGTGGC 60
 CCCGCGTCCT GAGCGCGCTC CAGCCTCCCA CGCGCGCCAC CCCGGGGTTC ACTGAGCCCC 120

GCGAGCCCGG GGAAGACAGA GAAAGAGAGG CCAGGGGGGG AACCCCATGG CCCGGCCCGT 180
 GTCCCGCACC CTGTGCGGTG GCCTCCTCCG GCACGGGGTC CCCGGGTCGC CTCCGGTCCC 240
 CGCGATCCGG ATGGCGCACG CAGTGGCTGG GGCCGGGCCG GGCTCGGGTG GTCGGAGGAG 300
 TCACCACTGA CCGGGTCATC TGGAGCCCGT GGCAGGCCGA GGCCCAGG 348

(2) INFORMATION FOR SEQ ID NO:14:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 87 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

TGCTACCTCA CGCCCCCGA CCTGCGAAAG GGCCCTCCCT GCCGACCCTC GCTGAGAACT 60
 GACTTCACAT AAAGTGTTGG AACTCCC 87

(2) INFORMATION FOR SEQ ID NO:15:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 19 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

Met Gln Arg Trp Lys Ala Ala Ala Leu Ala Ser Val Leu Cys Ser Ser
 1 5 10 15
 Val Leu Ser

(2) INFORMATION FOR SEQ ID NO:16:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 19 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

Met Arg Arg Trp Lys Ala Ala Ala Leu Val Ser Leu Ile Cys Ser Ser
 1 5 10 15
 Leu Leu Ser

(2) INFORMATION FOR SEQ ID NO:17:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 57 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

ATGCAGCGCT GGAAGCGGC GGCCTTGGCC TCAGTGCTCT GCAGCTCCGT GCTGTCC

57

(2) INFORMATION FOR SEQ ID NO:18:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 57 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

ATGAGGCGCT GGAAGGCAGC GGCCCTGGTG TCGCTCATCT GCAGCTCCCT GCTATCT

57

(2) INFORMATION FOR SEQ ID NO:19:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 76 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

Ile Trp Met Cys Arg Glu Gly Leu Leu Leu Ser His Arg Leu Gly Pro
 1 5 10 15
 Ala Leu Val Pro Leu His Arg Leu Pro Arg Thr Leu Asp Ala Arg Ile
 20 25 30
 Ala Arg Leu Ala Gln Tyr Arg Ala Leu Leu Gln Gly Ala Pro Asp Ala
 35 40 45
 Met Glu Leu Arg Glu Leu Thr Pro Trp Ala Gly Arg Pro Pro Gly Pro
 50 55 60
 Arg Arg Arg Ala Gly Pro Arg Arg Arg Ala Arg
 65 70 75

(2) INFORMATION FOR SEQ ID NO:20:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 228 base pairs

(B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

```

ATCTGGATGT GTCGAGAGGG CCTGCTTCTC AGCCACCGCC TCGGACCTGC GCTGGTCCCC      60
CTGCACCGCC TGCCTCGAAC CCTGGACGCC CGGATTGCCC GCCTGGCCCA GTACCGTGCA      120
CTCCTGCAGG GGGCCCCGGA TGCGATGGAG CTGCGCGAGC TGACGCCCTG GGCTGGGCGG      180
CCCCCAGGTC CGCGCCGTCG GCGGGGGCCC CGGCGGCGGC GCGCGCGT      228
  
```

(2) INFORMATION FOR SEQ ID NO:21:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 228 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:

```

GTCTGGATGT GCCAGGAGGG TCTGCTCTTG GGCCACCGCC TGGGACCCGC GCTTGCCCCG      60
CTACGACGCC CTCCACGCAC CCTGGACGCC CGCATCGCCC GCCTGGCCCA GTATCGCGCT      120
CTGCTCCAGG GCGCCCCCGA CGCGGTGGAG CTTGAGAAC TTTCTCCCTG GGCTGCCCCG      180
ATCCCGGGAC CGCGCCGTCG AGCGGGTCCC CGGCGTCGGC GGGCGCGG      228
  
```

(2) INFORMATION FOR SEQ ID NO:22:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 76 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:

```

Val Trp Met Cys Gln Glu Gly Leu Leu Gly His Arg Leu Gly Pro
 1             5             10             15
Ala Leu Ala Pro Leu Arg Arg Pro Pro Arg Thr Leu Asp Ala Arg Ile
      20             25             30
Ala Arg Leu Ala Gln Tyr Arg Ala Leu Leu Gln Gly Ala Pro Asp Ala
      35             40             45
Val Glu Leu Arg Glu Leu Ser Pro Trp Ala Ala Arg Ile Pro Gly Pro
      50             55             60
  
```

Arg Arg Arg Ala Gly Pro Arg Arg Arg Arg Ala Arg
 65 70 75

(2) INFORMATION FOR SEQ ID NO:23:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 95 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:23:

Met Gln Arg Trp Lys Ala Ala Ala Leu Ala Ser Val Leu Cys Ser Ser
 1 5 10 15
 Val Leu Ser Ile Trp Met Cys Arg Glu Gly Leu Leu Leu Ser His Arg
 20 25 30
 Leu Gly Pro Ala Leu Val Pro Leu His Arg Leu Pro Arg Thr Leu Asp
 35 40 45
 Ala Arg Ile Ala Arg Leu Ala Gln Tyr Arg Ala Leu Leu Gln Gly Ala
 50 55 60
 Pro Asp Ala Met Glu Leu Arg Glu Leu Thr Pro Trp Ala Gly Arg Pro
 65 70 75 80
 Pro Gly Pro Arg Arg Arg Ala Gly Pro Arg Arg Arg Arg Ala Arg
 85 90 95

(2) INFORMATION FOR SEQ ID NO:24:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 95 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:24:

Met Arg Arg Trp Lys Ala Ala Ala Leu Val Ser Leu Ile Cys Ser Ser
 1 5 10 15
 Leu Leu Ser Val Trp Met Cys Gln Glu Gly Leu Leu Leu Gly His Arg
 20 25 30
 Leu Gly Pro Ala Leu Ala Pro Leu Arg Arg Pro Pro Arg Thr Leu Asp
 35 40 45
 Ala Arg Ile Ala Arg Leu Ala Gln Tyr Arg Ala Leu Leu Gln Gly Ala
 50 55 60
 Pro Asp Ala Val Glu Leu Arg Glu Leu Ser Pro Trp Ala Ala Arg Ile
 65 70 75 80
 Pro Gly Pro Arg Arg Arg Ala Gly Pro Arg Arg Arg Arg Ala Arg
 85 90 95

(2) INFORMATION FOR SEQ ID NO:25:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 285 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:25:

```

ATGCAGCGCT GGAAGGCGGC GGCCTTGGCC TCAGTGCTCT GCAGCTCCGT GCTGTCCATC      60
TGGATGTGTC GAGAGGGCCT GCTTCTCAGC CACCGCCTCG GACCTGCGCT GGTCCCCCTG      120
CACCGCCTGC CTCGAACCCT GGACGCCCGG ATTGCCCGCC TGGCCCAGTA CCGTGCACTC      180
CTGCAGGGGG CCCCGGATGC GATGGAGCTG CGCGAGCTGA CGCCCTGGGC TGGGCGGGCC      240
CCAGGTCCGC GCCGTCGGGC GGGGCCCCGG CGGCGGCGCG CGCGT      285

```

(2) INFORMATION FOR SEQ ID NO:26:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 285 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:26:

```

ATGAGGCGCT GGAAGGCAGC GGCCCTGGTG TCGCTCATCT GCAGCTCCCT GCTATCTGTC      60
TGGATGTGCC AGGAGGGTCT GCTCTTGGGC CACCGCCTGG GACCCGCGCT TGCCCCGCTA      120
CGACGCCCTC CACGCACCCT GGACGCCCGC ATCGCCCGCC TGGCCCAGTA TCGCGCTCTG      180
CTCCAGGGCG CCCCCGACGC GGTGGAGCTT CGAGAACTTT CTCCCTGGGC TGCCCCGATC      240
CCGGGACCGC GCCGTCGAGC GGGTCCCCGG CGTCGGCGGG CGCGG      285

```

(2) INFORMATION FOR SEQ ID NO:27:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 169 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:27:

```

ATGCAGCGCT GGAAGGCGGC GGCCTTGGCC TCAGTGCTCT GCAGCTCCGT GCTGTCCATC      60
TGGATGTGTC GAGAGGGCCT GCTTCTCAGC CACCGCCTCG GACCTGCGCT GGTCCCCCTG      120

```

CACCGCCTGC CTCGAACCCT GGACGCCCGG ATTGCCCGCC TGGCCCAGT

169

(2) INFORMATION FOR SEQ ID NO:28:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 425 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:28:

| | |
|--|-----|
| ACCGTGCACT CCTGCAGGGG GCCCCGGATG CGATGGAGCT GCGCGAGCTG ACGCCCTGGG | 60 |
| CTGGGCGGGC CCCAGGTCCG CGCCGTCGGG CGGGGCCCCG GCGGCGGCGC GCGCGTGCGC | 120 |
| GGTTGGGGGC GCGGCCTTGC GGGCTGCGCG AGCTGGAGGT GCGCGTGAGC GAGCTGGGCC | 180 |
| TGGGCTACGC GTCCGACGAG ACGGTGCTGT TCCGCTACTG CGCAGGCGCC TGCAGAGGCTG | 240 |
| CCGCGCGCGT CTACGACCTC GGGCTGCGAC GACTGCGCCA GCGGCGGCGC CTGCGGCGGG | 300 |
| AGCGGGTGCG CGCGCAGCCC TGCTGCCGCC CGACGGCCTA CGAGGACGAG GTGTCCTTCC | 360 |
| TGGACGCGCA CAGCCGCTAC CACACGGTGC ACGAGCTGTC GCGCGCGAG TCGCCTGCG | 420 |
| TGTGA | 425 |

(2) INFORMATION FOR SEQ ID NO:29:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 169 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:29:

| | |
|---|-----|
| ATGAGGCGCT GGAAGGCAGC GGCCCTGGTG TCGCTCATCT GCAGCTCCCT GCTATCTGTC | 60 |
| TGGATGTGCC AGGAGGTCT GCTCTTGGGC CACCGCTGG GACCCGCGCT TGCCCCGCTA | 120 |
| CGACGCCCTC CACGCACCCT GGACGCCCGC ATCGCCCGCC TGGCCCAGT | 169 |

(2) INFORMATION FOR SEQ ID NO:30:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 419 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:30:

```

ATCGCGCTCT GCTCCAGGGC GCCCCGACG CGGTGGAGCT TCGAGAACTT TCTCCCTGGG      60
CTGCCCCGAT CCCGGGACCG CGCCGTCGAG CGGGTCCCCG GCGTCGGCGG GCGCGGCCCG      120
GGGCTCGGCC TTGTGGGCTG CGCGAGCTCG AGGTGCGCGT GAGCGAGCTG GGCCTGGGCT      180
ACACGTCGGA TGAGACCGTG CTGTTCCGCT ACTGCGCAGG CGCGTGCGAG GCGGCCATCC      240
GCATCTACGA CCTGGGCCTT CGGCGCCTGC GCCAGCGGAG GCGCGTGCGC AGAGAGCGGG      300
CGCGGGCGCA CCCGTGTTGT CGCCCGACGG CCTATGAGGA CGAGGTGTCC TTCCTGGACG      360
TGCACAGCCG CTACCACACG CTGCAAGAGC TGTCGGCGCG GGAGTGCGCG TCGTGTGA      419

```

(2) INFORMATION FOR SEQ ID NO:31:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 94 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:31:

```

Cys Gly Leu Arg Glu Leu Glu Val Arg Val Ser Glu Leu Gly Leu Gly
1           5           10           15
Tyr Ala Ser Asp Glu Thr Val Leu Phe Arg Tyr Cys Ala Gly Ala Cys
20          25          30
Glu Ala Ala Ala Arg Val Tyr Asp Leu Gly Leu Arg Arg Leu Arg Gln
35          40          45
Arg Arg Arg Leu Arg Arg Glu Arg Val Arg Ala Gln Pro Cys Cys Arg
50          55          60
Pro Thr Ala Tyr Glu Asp Glu Val Ser Phe Leu Asp Ala His Ser Arg
65          70          75          80
Tyr His Thr Val His Glu Leu Ser Ala Arg Glu Cys Ala Cys
85          90

```

(2) INFORMATION FOR SEQ ID NO:32:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 94 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:32:

```

Cys Gly Leu Arg Glu Leu Glu Val Arg Val Ser Glu Leu Gly Leu Gly
1           5           10           15

```

Tyr Thr Ser Asp Glu Thr Val Leu Phe Arg Tyr Cys Ala Gly Ala Cys
 20 25 30
 Glu Ala Ala Ile Arg Ile Tyr Asp Leu Gly Leu Arg Arg Leu Arg Gln
 35 40 45
 Arg Arg Arg Val Arg Arg Glu Arg Ala Arg Ala His Pro Cys Cys Arg
 50 55 60
 Pro Thr Ala Tyr Glu Asp Glu Val Ser Phe Leu Asp Val His Ser Arg
 65 70 75 80
 Tyr His Thr Leu Gln Glu Leu Ser Ala Arg Glu Cys Ala Cys
 85 90

(2) INFORMATION FOR SEQ ID NO:33:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 8 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 2
- (D) OTHER INFORMATION: /note= "SERINE OR THREONINE"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 3
- (D) OTHER INFORMATION: /note= "GLUTAMIC ACID OR ASPARTIC

ACID"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:33:

Val Xaa Xaa Leu Gly Leu Gly Tyr
 1 5

(2) INFORMATION FOR SEQ ID NO:34:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 15 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 2
- (D) OTHER INFORMATION: /note= "THREONINE OR GLUTAMIC ACID"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 3
- (D) OTHER INFORMATION: /note= "VALINE OR LEUCINE"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site

(B) LOCATION: 4
 (D) OTHER INFORMATION: /note= "LEUCINE OR ISOLEUCINE"

(ix) FEATURE:
 (A) NAME/KEY: Modified-site
 (B) LOCATION: 9
 (D) OTHER INFORMATION: /note= "ALANINE OR SERINE"

(ix) FEATURE:
 (A) NAME/KEY: Modified-site
 (B) LOCATION: 11
 (D) OTHER INFORMATION: /note= "ALANINE OR SERINE"

(ix) FEATURE:
 (A) NAME/KEY: Modified-site
 (B) LOCATION: 13
 (D) OTHER INFORMATION: /note= "GLUTAMIC ACID OR ASPARTIC
 ACID"

(ix) FEATURE:
 (A) NAME/KEY: Modified-site
 (B) LOCATION: 14
 (D) OTHER INFORMATION: /note= "ALANINE OR SERINE"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:34:

| | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Glu | Xaa | Xaa | Xaa | Phe | Arg | Tyr | Cys | Xaa | Gly | Xaa | Cys | Xaa | Xaa | Ala |
| 1 | | | | 5 | | | | | 10 | | | | | 15 |

(2) INFORMATION FOR SEQ ID NO:35:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 15 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:
 (A) NAME/KEY: Modified-site
 (B) LOCATION: 5
 (D) OTHER INFORMATION: /note= "THREONINE OR VALINE OR
 ISOLEUCINE"

(ix) FEATURE:
 (A) NAME/KEY: Modified-site
 (B) LOCATION: 7
 (D) OTHER INFORMATION: /note= "TYROSINE OR PHENYLALANINE"

(ix) FEATURE:
 (A) NAME/KEY: Modified-site
 (B) LOCATION: 8
 (D) OTHER INFORMATION: /note= "GLUTAMIC ACID OR ASPARTIC
 ACID"

(ix) FEATURE:
 (A) NAME/KEY: Modified-site
 (B) LOCATION: 10
 (D) OTHER INFORMATION: /note= "GLUTAMIC ACID OR ASPARTIC
 ACID"

(ix) FEATURE:
 (A) NAME/KEY: Modified-site

- (B) LOCATION: 11
- (D) OTHER INFORMATION: /note= "VALINE OR LEUCINE"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:35:

| | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Cys | Cys | Arg | Pro | Xaa | Ala | Xaa | Xaa | Asp | Xaa | Xaa | Ser | Phe | Leu | Asp |
| 1 | | | | 5 | | | | 10 | | | | | 15 | |

(2) INFORMATION FOR SEQ ID NO:36:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 11 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

- (ix) FEATURE:
 - (A) NAME/KEY: Modified-site
 - (B) LOCATION: 5
 - (D) OTHER INFORMATION: /note= "ALANINE OR SERINE"

- (ix) FEATURE:
 - (A) NAME/KEY: Modified-site
 - (B) LOCATION: 7
 - (D) OTHER INFORMATION: /note= "ALANINE OR SERINE"

- (ix) FEATURE:
 - (A) NAME/KEY: Modified-site
 - (B) LOCATION: 9
 - (D) OTHER INFORMATION: /note= "GLUTAMIC ACID OR ASPARTIC

ACID"

- (ix) FEATURE:
 - (A) NAME/KEY: Modified-site
 - (B) LOCATION: 10
 - (D) OTHER INFORMATION: /note= "SERINE OR ALANINE"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:36:

| | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Phe | Arg | Tyr | Cys | Xaa | Gly | Xaa | Cys | Xaa | Xaa | Ala |
| 1 | | | | 5 | | | | 10 | | |

(2) INFORMATION FOR SEQ ID NO:37:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 11 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

- (ix) FEATURE:
 - (A) NAME/KEY: Modified-site
 - (B) LOCATION: 5
 - (D) OTHER INFORMATION: /note= "ALANINE OR SERINE"

- (ix) FEATURE:
 - (A) NAME/KEY: Modified-site
 - (B) LOCATION: 7

(D) OTHER INFORMATION: /note= "ALANINE OR SERINE"

(ix) FEATURE:

(A) NAME/KEY: Modified-site

(B) LOCATION: 9

(D) OTHER INFORMATION: /note= "GLUTAMIC ACID OR ASPARTIC ACID"

(ix) FEATURE:

(A) NAME/KEY: Modified-site

(B) LOCATION: 10

(D) OTHER INFORMATION: /note= "SERINE OR ALANINE"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:37:

| | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Phe | Arg | Tyr | Cys | Xaa | Gly | Xaa | Cys | Xaa | Xaa | Ala |
| 1 | | | | 5 | | | | | | 10 |

(2) INFORMATION FOR SEQ ID NO:38:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 10 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: Modified-site

(B) LOCATION: 5

(D) OTHER INFORMATION: /note= "ISOLEUCINE OR THREONINE OR VALINE"

(ix) FEATURE:

(A) NAME/KEY: Modified-site

(B) LOCATION: 7

(D) OTHER INFORMATION: /note= "TYROSINE OR PHENYLALANINE"

(ix) FEATURE:

(A) NAME/KEY: Modified-site

(B) LOCATION: 8

(D) OTHER INFORMATION: /note= "GLUTAMIC ACID OR ASPARTIC ACID"

(ix) FEATURE:

(A) NAME/KEY: Modified-site

(B) LOCATION: 10

(D) OTHER INFORMATION: /note= "GLUTAMIC ACID OR ASPARTIC ACID"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:38:

| | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Cys | Cys | Arg | Pro | Xaa | Ala | Xaa | Xaa | Asp | Xaa |
| 1 | | | | 5 | | | | | 10 |

(2) INFORMATION FOR SEQ ID NO:39:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 10 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 2
- (D) OTHER INFORMATION: /note= "TYROSINE OR PHENYLALANINE"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 3
- (D) OTHER INFORMATION: /note= "GLUTAMIC ACID OR ASPARTIC

ACID"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 5
- (D) OTHER INFORMATION: /note= "GLUTAMIC ACID OR ASPARTIC

ACID"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 6
- (D) OTHER INFORMATION: /note= "VALINE OR LEUCINE"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:39:

| | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Ala | Xaa | Xaa | Asp | Xaa | Xaa | Ser | Phe | Leu | Asp |
| 1 | | | | 5 | | | | 10 | |

(2) INFORMATION FOR SEQ ID NO:40:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 8 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 2
- (D) OTHER INFORMATION: /note= "GLUTAMIC ACID OR THREONINE"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 3
- (D) OTHER INFORMATION: /note= "LEUCINE OR VALINE"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 4
- (D) OTHER INFORMATION: /note= "ISOLEUCINE OR LEUCINE"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:40:

| | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|
| Glu | Xaa | Xaa | Xaa | Phe | Arg | Tyr | Cys |
| 1 | | | | 5 | | | |

(2) INFORMATION FOR SEQ ID NO:41:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 13 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:
 (A) NAME/KEY: Modified-site
 (B) LOCATION: 2
 (D) OTHER INFORMATION: /note= "GLUTAMIC ACID OR THREONINE"

(ix) FEATURE:
 (A) NAME/KEY: Modified-site
 (B) LOCATION: 3
 (D) OTHER INFORMATION: /note= "LEUCINE OR VALINE"

(ix) FEATURE:
 (A) NAME/KEY: Modified-site
 (B) LOCATION: 4
 (D) OTHER INFORMATION: /note= "ISOLEUCINE OR LEUCINE"

(ix) FEATURE:
 (A) NAME/KEY: Modified-site
 (B) LOCATION: 9
 (D) OTHER INFORMATION: /note= "SERINE OR ALANINE"

(ix) FEATURE:
 (A) NAME/KEY: Modified-site
 (B) LOCATION: 11
 (D) OTHER INFORMATION: /note= "SERINE OR ALANINE"

(ix) FEATURE:
 (A) NAME/KEY: Modified-site
 (B) LOCATION: 13
 (D) OTHER INFORMATION: /note= "GLUTAMIC ACID OR ASPARTIC
 ACID"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:41:

| | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Glu | Xaa | Xaa | Xaa | Phe | Arg | Tyr | Cys | Xaa | Gly | Xaa | Cys | Xaa |
| 1 | | | | 5 | | | | | 10 | | | |

(2) INFORMATION FOR SEQ ID NO:42:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 23 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:42:

GTNWSNGANY TNGGNYTNGG NTA

23

(2) INFORMATION FOR SEQ ID NO:43:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 32 base pairs

(B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:43:

TTYMGNTAYT GYDSNGGND S NTGYGANKCN GC

32

(2) INFORMATION FOR SEQ ID NO:44:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 32 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:44:

GCNGMNTCRC ANSHNCCNSH RCARTANCKR AA

32

(2) INFORMATION FOR SEQ ID NO:45:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 29 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:45:

TCRTCNTCRW ANGCMRYNGG NCKRCARCA

29

(2) INFORMATION FOR SEQ ID NO:46:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 29 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:46:

TCNARRAANS WNAVNTCR TC NTCRWANGC

29

(2) INFORMATION FOR SEQ ID NO:47:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 23 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single

(D) TOPOLOGY: linear
 (ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:47:

GARRMNBTHN TNTTYMGNTA YTG

23

(2) INFORMATION FOR SEQ ID NO:48:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 38 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:48:

GARRMNBTHN TNTTYMGNTA YTGYSNGGN DSNTGHGA

38

(2) INFORMATION FOR SEQ ID NO:49:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 1023 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:49:

| | |
|--|-----|
| GGAGGGAGAG CGCGCGGTGG TTTCGTCCGT GTGCCCCGCG CCCGGCGCTC CTCGCGTGGC | 60 |
| CCCGCGTCCCT GAGCGCGCTC CAGCCTCCCA CGCGCGCCAC CCCGGGGTTC ACTGAGCCCG | 120 |
| GCGAGCCCGG GGAAGACAGA GAAAGAGAGG CCAGGGGGGG AACCCCATGG CCCGGCCCGT | 180 |
| GTCCCGCACC CTGTGCGGTG GCCTCCTCCG GCACGGGGTC CCCGGGTCGC CTCCGGTCCC | 240 |
| CGCGATCCGG ATGGCGCACG CAGTGGCTGG GGCCGGGGCC GGCTCGGGTG GTCGGAGGAG | 300 |
| TCACCACTGA CCGGGTCATC TGGAGCCCGT GGCAGGCCGA GGCCAGGAT GAGGCGCTGG | 360 |
| AAGGCAGCGG CCCTGGTGTC GCTCATCTGC AGCTCCCTGC TATCTGTCTG GATGTGCCAG | 420 |
| GAGGGTCTGC TCTTGGGCCA CCGCCTGGGA CCCGCGCTTG CCCGCTACG ACGCCCTCCA | 480 |
| CGCACCTTGG ACGCCCGCAT CGCCCGCCTG GCCAGTATC GCGCTCTGCT CCAGGGCGCC | 540 |
| CCCACGCGG TGGAGCTTCG AGAACTTTCT CCCTGGGCTG CCCGCATCCC GGGACCGCGC | 600 |
| CGTCGAGCGG GTCCCCGGCG TCGGCGGGCG CGGCCGGGGG CTCGGCCTTG TGGGCTGCGC | 660 |
| GAGCTCGAGG TGCGCGTGAG CGAGCTGGGC CTGGGCTACA CGTCGGATGA GACCGTGCTG | 720 |
| TTCCGCTACT GCGCAGGCGC GTGCGAGGCG GCCATCCGCA TCTACGACCT GGGCCTTCGG | 780 |

CGCCTGCGCC AGCGGAGGCG CGTGCGCAGA GAGCGGGCGC GGGCGCACCC GTGTTGTCGC 840
 CCGACGGCCT ATGAGGACGA GGTGTCCTTC CTGGACGTGC ACAGCCGCTA CCACACGCTG 900
 CAAGAGCTGT CGGCGCGGGA GTGCGCGTGC GTGTGATGCT ACCTCACGCC CCCCACCTG 960
 CGAAAGGGCC CTCCCTGCCG ACCCTCGCTG AGAACTGACT TCACATAAAG TGTGGGAACT 1020
 CCC 1023

(2) INFORMATION FOR SEQ ID NO:50:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 17 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:50:

CCNACNGCNT AYGARGA

17

(2) INFORMATION FOR SEQ ID NO:51:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 93 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:51:

Cys Val Leu Thr Ala Ile His Leu Asn Val Thr Asp Leu Gly Leu Gly
 1 5 10 15
 Tyr Glu Thr Lys Glu Glu Leu Ile Phe Arg Tyr Cys Ser Gly Ser Cys
 20 25 30
 Asp Ala Ala Glu Thr Thr Tyr Asp Lys Ile Leu Lys Asn Leu Ser Arg
 35 40 45
 Asn Arg Arg Leu Val Ser Asp Lys Val Gly Gln Ala Cys Cys Arg Pro
 50 55 60
 Ile Ala Phe Asp Asp Asp Leu Ser Phe Leu Asp Asp Asn Leu Val Tyr
 65 70 75 80
 His Ile Leu Arg Lys His Ser Ala Lys Arg Cys Gly Cys
 85 90

(2) INFORMATION FOR SEQ ID NO:52:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid

(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:52:

ARYTCYTGNA RNGTRTGRTA

20

(2) INFORMATION FOR SEQ ID NO:53:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 28 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:53:

GACGAGGTGT CCTTCCTGGA CGTACACA

28

(2) INFORMATION FOR SEQ ID NO:54:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 34 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:54:

TAGCGGCTGT GTACGTCCAG GAAGGACACC TCGT

34

(2) INFORMATION FOR SEQ ID NO:55:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 26 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:55:

CAGCGACGAC GCGTGCACAA AGAGCG

26

(2) INFORMATION FOR SEQ ID NO:56:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 47 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:56:

TAYGARGACG AGGTGTCCTT CCTGGACGTA CACAGCCGCT AYCAYAC

47

(2) INFORMATION FOR SEQ ID NO:57:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 26 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:57:

GCGGCCATCC GCATCTACGA CCTGGG

26

(2) INFORMATION FOR SEQ ID NO:58:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 27 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:58:

CRTAGGCCGT CGGGCGRCAR CACGGGT

27

(2) INFORMATION FOR SEQ ID NO:59:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 27 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:59:

GCGCCGAAGG CCCAGGTCGT AGATGCG

27

(2) INFORMATION FOR SEQ ID NO:60:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 29 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:60:

CGCTACTGCG CAGGCGCGTG CGARGCGGC

29

(2) INFORMATION FOR SEQ ID NO:61:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 27 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:61:

CGCCGACAGC TCTTGCAGCG TRTGGA

27

(2) INFORMATION FOR SEQ ID NO:62:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 30 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:62:

GAGCTGGGCC TGGGCTACGC GTCCGACGAG

30

(2) INFORMATION FOR SEQ ID NO:63:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 39 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:63:

GCGACGCGTA CCATGAGGCG CTGGAAGGCA GCGGCCCTG

39

(2) INFORMATION FOR SEQ ID NO:64:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 30 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:64:

GACGGATCCG CATCACACGC ACGCGCACTC

30

(2) INFORMATION FOR SEQ ID NO:65:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 29 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:65:

GACCATATGC CGGGGGCTCG GCCTTGTGG

29

(2) INFORMATION FOR SEQ ID NO:66:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 30 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:66:

GACGGATCCG CATCACACGC ACGCGCACTC

30

(2) INFORMATION FOR SEQ ID NO:67:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 26 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:67:

CAGCGACGAC GCGTGCGCAA AGAGCG

26

(2) INFORMATION FOR SEQ ID NO:68:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 34 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:68:

TAGCGGCTGT GTACGTCCAG GAAGGACACC TCGT

34

(2) INFORMATION FOR SEQ ID NO:69:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 21 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:69:

AAAAATCGGG GGTGYGTCTT A

21

(2) INFORMATION FOR SEQ ID NO:70:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 21 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:70:

CATGCCTGGC CTACYTTGTC A

21

(2) INFORMATION FOR SEQ ID NO:71:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 24 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:71:

CTGGCGTCCC AMCAAGGGTC TTCG

24

(2) INFORMATION FOR SEQ ID NO:72:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 23 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:72:

GCCAGTGGTG CCGTCGAGGC GGG

23

(2) INFORMATION FOR SEQ ID NO:73:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 24 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:73:

GGCCCAGGAT GAGGCGCTGG AAGG

24

(2) INFORMATION FOR SEQ ID NO:74:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 27 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:74:

CCACTCCACT GCCTGAWATT CWACCCC

27

(2) INFORMATION FOR SEQ ID NO:75:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 24 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:75:

CCATGTGATT ATCGACCATT CGGC

24

(2) INFORMATION FOR SEQ ID NO:76:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 134 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:76:

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Ser | Pro | Asp | Lys | Gln | Met | Ala | Val | Leu | Pro | Arg | Arg | Glu | Arg | Asn | Arg |
| 1 | | | | 5 | | | | 10 | | | | | | 15 | |

Gln Ala Ala Ala Ala Asn Pro Glu Asn Ser Arg Gly Lys Gly Arg Arg
 20 25 30
 Gly Gln Arg Gly Lys Asn Arg Gly Cys Val Leu Thr Ala Ile His Leu
 35 40 45
 Asn Val Thr Asp Leu Gly Leu Gly Tyr Glu Thr Lys Glu Glu Leu Ile
 50 55 60
 Phe Arg Tyr Cys Ser Gly Ser Cys Asp Ala Ala Glu Thr Thr Tyr Asp
 65 70 75 80
 Lys Ile Leu Lys Asn Leu Ser Arg Asn Arg Arg Leu Val Ser Asp Lys
 85 90 95
 Val Gly Gln Ala Cys Cys Arg Pro Ile Ala Phe Asp Asp Asp Leu Ser
 100 105 110
 Phe Leu Asp Asp Asn Leu Val Tyr His Ile Leu Arg Lys His Ser Ala
 115 120 125
 Lys Arg Cys Gly Cys Ile
 130

(2) INFORMATION FOR SEQ ID NO:77:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 134 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:77:

Ser Pro Asp Lys Gln Ala Ala Ala Leu Pro Arg Arg Glu Arg Asn Arg
 1 5 10 15
 Gln Ala Ala Ala Ala Ser Pro Glu Asn Ser Arg Gly Lys Gly Arg Arg
 20 25 30
 Gly Gln Arg Gly Lys Asn Arg Gly Cys Val Leu Thr Ala Ile His Leu
 35 40 45
 Asn Val Thr Asp Leu Gly Leu Gly Tyr Glu Thr Lys Glu Glu Leu Ile
 50 55 60
 Phe Arg Tyr Cys Ser Gly Ser Cys Glu Ser Ala Glu Thr Met Tyr Asp
 65 70 75 80
 Lys Ile Leu Lys Asn Leu Ser Arg Ser Arg Arg Leu Thr Ser Asp Lys
 85 90 95
 Val Gly Gln Ala Cys Cys Arg Pro Val Ala Phe Asp Asp Asp Leu Ser
 100 105 110
 Phe Leu Asp Asp Asn Leu Val Tyr His Ile Leu Arg Lys His Ser Ala
 115 120 125
 Lys Arg Cys Gly Cys Ile
 130

(2) INFORMATION FOR SEQ ID NO:78:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 134 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:78:

```

Ser Pro Asp Lys Gln Ala Ala Ala Leu Pro Arg Arg Glu Arg Asn Arg
1      5      10      15
Gln Ala Ala Ala Ala Ser Pro Glu Asn Ser Arg Gly Lys Gly Arg Arg
20      25      30
Gly Gln Arg Gly Lys Asn Arg Gly Cys Val Leu Thr Ala Ile His Leu
35      40      45
Asn Val Thr Asp Leu Gly Leu Gly Tyr Glu Thr Lys Glu Glu Leu Ile
50      55      60
Phe Arg Tyr Cys Ser Gly Ser Cys Glu Ala Ala Glu Thr Met Tyr Asp
65      70      75      80
Lys Ile Leu Lys Asn Leu Ser Arg Ser Arg Arg Leu Thr Ser Asp Lys
85      90      95
Val Gly Gln Ala Cys Cys Arg Pro Val Ala Phe Asp Asp Asp Leu Ser
100     105     110
Phe Leu Asp Asp Ser Leu Val Tyr His Ile Leu Arg Lys His Ser Ala
115     120     125
Lys Arg Cys Gly Cys Ile
130

```

(2) INFORMATION FOR SEQ ID NO:79:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 89 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:79:

```

Cys Arg Leu Trp Ser Leu Thr Leu Pro Val Ala Glu Leu Gly Leu Gly
1      5      10      15
Tyr Ala Ser Glu Lys Val Ile Phe Arg Tyr Cys Ala Gly Ser Cys
20      25      30
Pro Gln Glu Ala Arg Thr Gln His Ser Leu Val Leu Ala Arg Leu Arg
35      40      45

```

Gly Arg Gly Arg Ala His Gly Arg Pro Cys Cys Gln Pro Thr Ser Tyr
 50 55 60
 Ala Asp Val Thr Phe Leu Asp Asp Gln His His Trp Gln Gln Leu Pro
 65 70 75 80
 Gln Leu Ser Ala Ala Ala Cys Gly Cys
 85

(2) INFORMATION FOR SEQ ID NO:80:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 96 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:80:

Ala Leu Ala Gly Ser Cys Arg Leu Trp Ser Leu Thr Leu Pro Val Ala
 1 5 10 15
 Glu Leu Gly Leu Gly Tyr Ala Ser Glu Glu Lys Val Ile Phe Arg Tyr
 20 25 30
 Cys Ala Gly Ser Cys Pro Gln Glu Ala Arg Thr Gln His Ser Leu Val
 35 40 45
 Leu Ala Arg Leu Arg Gly Arg Gly Arg Ala His Gly Arg Pro Cys Cys
 50 55 60
 Gln Pro Thr Ser Tyr Ala Asp Val Thr Phe Leu Asp Asp Gln His His
 65 70 75 80
 Trp Gln Gln Leu Pro Gln Leu Ser Ala Ala Ala Cys Gly Cys Gly Gly
 85 90 95

(2) INFORMATION FOR SEQ ID NO:81:

- (i) SEQUENCE CHARACTERISTICS:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:81:

This sequence is intentionally skipped.

(2) INFORMATION FOR SEQ ID NO:82:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 89 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:82:

Cys Arg Leu Trp Ser Leu Thr Leu Pro Val Ala Glu Leu Gly Leu Gly
 1 5 10 15
 Tyr Ala Ser Glu Glu Lys Ile Ile Phe Arg Tyr Cys Ala Gly Ser Cys
 20 25 30
 Pro Gln Glu Val Arg Thr Gln His Ser Leu Val Leu Ala Arg Leu Arg
 35 40 45
 Gly Gln Gly Arg Ala His Gly Arg Pro Cys Cys Gln Pro Thr Ser Tyr
 50 55 60
 Ala Asp Val Thr Phe Leu Asp Asp His His His Trp Gln Gln Leu Pro
 65 70 75 80
 Gln Leu Ser Ala Ala Ala Cys Gly Cys
 85

(2) INFORMATION FOR SEQ ID NO:83:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 91 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:83:

Cys Arg Leu Trp Ser Leu Thr Leu Pro Val Ala Glu Leu Gly Leu Gly
 1 5 10 15
 Tyr Ala Ser Glu Glu Lys Ile Ile Phe Arg Tyr Cys Ala Gly Ser Cys
 20 25 30
 Pro Gln Glu Val Arg Thr Gln His Ser Leu Val Leu Ala Arg Leu Arg
 35 40 45
 Gly Gln Gly Arg Ala His Gly Arg Pro Cys Cys Gln Pro Thr Ser Tyr
 50 55 60
 Ala Asp Val Thr Phe Leu Asp Asp His His His Trp Gln Gln Leu Pro
 65 70 75 80
 Gln Leu Ser Ala Ala Ala Cys Gly Cys Gly Gly
 85 90

(2) INFORMATION FOR SEQ ID NO:84:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 267 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:84:

| | |
|---|-----|
| TGCCGACTGT GGAGCCTGAC CCTACCACTG GCTGAGCTGG GCCTGGGCTA TGCCTCGGAG | 60 |
| GAGAAGGTCA TCTTCCGATA CTGTGCTGGC AGCTGTCCCC AAGAGGCCCG TACCCAGCAC | 120 |
| AGTCTGGTAC TGGCCCGGCT TCGAGGGCGG GGTGAGCCC ATGGCCGACC CTGCTGCCAG | 180 |
| CCCACCAGCT ATGCTGATGT GACCTTCCTT GATGATCAGC ACCATTGGCA GCAGCTGCCT | 240 |
| CAGCTCTCAG CTGCAGCTTG TGGCTGT | 267 |

(2) INFORMATION FOR SEQ ID NO:85:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 267 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:85:

| | |
|---|-----|
| TGCCGGCTGT GGAGCCTGAC CCTACCACTG GCTGAGCTTG GCCTGGGCTA TGCCTCAGAG | 60 |
| GAGAAGATTA TCTTCCGATA CTGTGCTGGC AGCTGTCCCC AAGAGGTCCG TACCCAGCAC | 120 |
| AGTCTGGTGC TGGCCCGTCT TCGAGGGCAG GGTGAGCTC ATGGCAGACC TTGCTGCCAG | 180 |
| CCCACCAGCT ATGCTGATGT GACCTTCCTT GATGACCACC ACCATTGGCA GCAGCTGCCT | 240 |
| CAGCTCTCAG CCGCAGCTTG TGGCTGT | 267 |

(2) INFORMATION FOR SEQ ID NO:86:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 273 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:86:

| | |
|---|-----|
| TGCCGGCTGT GGAGCCTGAC CCTACCACTG GCTGAGCTTG GCCTGGGCTA TGCCTCAGAG | 60 |
| GAGAAGATTA TCTTCCGATA CTGTGCTGGC AGCTGTCCCC AAGAGGTCCG TACCCAGCAC | 120 |
| AGTCTGGTGC TGGCCCGTCT TCGAGGGCAG GGTGAGCTC ATGGCAGACC TTGCTGCCAG | 180 |
| CCCACCAGCT ATGCTGATGT GACCTTCCTT GATGACCACC ACCATTGGCA GCAGCTGCCT | 240 |
| CAGCTCTCAG CCGCAGCTTG TGGCTGTGGT GGC | 273 |

(2) INFORMATION FOR SEQ ID NO:87:

- (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 94 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:87:

| | | | | | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|----|----|----|----|
| Cys | Val | Leu | Thr | Ala | Ile | His | Leu | Asn | Val | Thr | Asp | Leu | Gly | Leu | Gly | 1 | 5 | 10 | 15 |
| Tyr | Glu | Thr | Lys | Glu | Glu | Leu | Ile | Phe | Arg | Tyr | Cys | Ser | Gly | Ser | Cys | 20 | 25 | 30 | |
| Glu | Ser | Ala | Glu | Thr | Met | Tyr | Asp | Lys | Ile | Leu | Lys | Asn | Leu | Ser | Arg | 35 | 40 | 45 | |
| Ser | Arg | Arg | Leu | Thr | Ser | Asp | Lys | Val | Gly | Gln | Ala | Cys | Cys | Arg | Pro | 50 | 55 | 60 | |
| Val | Ala | Phe | Asp | Asp | Asp | Leu | Ser | Phe | Leu | Asp | Asp | Asn | Leu | Val | Tyr | 65 | 70 | 75 | 80 |
| His | Ile | Leu | Arg | Lys | His | Ser | Ala | Lys | Arg | Cys | Gly | Cys | Ile | 85 | 90 | | | | |

(2) INFORMATION FOR SEQ ID NO:88:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 95 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:88:

| | | | | | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|----|----|----|----|
| Cys | Gly | Leu | Arg | Glu | Leu | Glu | Val | Arg | Val | Ser | Glu | Leu | Gly | Leu | Gly | 1 | 5 | 10 | 15 |
| Tyr | Thr | Ser | Asp | Glu | Thr | Val | Leu | Phe | Arg | Tyr | Cys | Ala | Gly | Ala | Cys | 20 | 25 | 30 | |
| Glu | Ala | Ala | Ile | Arg | Ile | Tyr | Asp | Leu | Gly | Leu | Arg | Arg | Leu | Arg | Gln | 35 | 40 | 45 | |
| Arg | Arg | Arg | Val | Arg | Arg | Glu | Arg | Ala | Arg | Ala | His | Pro | Cys | Cys | Arg | 50 | 55 | 60 | |
| Pro | Thr | Ala | Tyr | Glu | Asp | Glu | Val | Ser | Phe | Leu | Asp | Val | His | Ser | Arg | 65 | 70 | 75 | 80 |
| Tyr | His | Thr | Leu | Gln | Glu | Leu | Ser | Ala | Arg | Glu | Cys | Ala | Cys | Val | 85 | 90 | 95 | | |

(2) INFORMATION FOR SEQ ID NO:89:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 91 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:89:

```

Cys Arg Leu Trp Ser Leu Thr Leu Pro Val Ala Glu Leu Gly Leu Gly
1      5      10      15
Tyr Ala Ser Glu Glu Lys Val Ile Phe Arg Tyr Cys Ala Gly Ser Cys
20      25      30
Pro Gln Glu Ala Arg Thr Gln His Ser Leu Val Leu Ala Arg Leu Arg
35      40      45
Gly Arg Gly Arg Ala His Gly Arg Pro Cys Cys Gln Pro Thr Ser Tyr
50      55      60
Ala Asp Val Thr Phe Leu Asp Asp Gln His His Trp Gln Gln Leu Pro
65      70      75      80
Gln Leu Ser Ala Ala Ala Cys Gly Cys Gly Gly
85      90

```

(2) INFORMATION FOR SEQ ID NO:90:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 22 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:90:

TGCCTCAGAG GAGAAGATTA TC

22

(2) INFORMATION FOR SEQ ID NO:91:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 7 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:91:

```

Ala Ser Glu Glu Lys Ile Ile
1      5

```

(2) INFORMATION FOR SEQ ID NO:92:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 16 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:92:

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Leu | Gly | Leu | Gly | Tyr | Glu | Thr | Lys | Glu | Glu | Leu | Ile | Phe | Arg | Tyr | Cys |
| 1 | | | | 5 | | | | 10 | | | | | | 15 | |

(2) INFORMATION FOR SEQ ID NO:93:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 16 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:93:

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Leu | Gly | Leu | Gly | Tyr | Thr | Ser | Asp | Glu | Thr | Val | Leu | Phe | Arg | Tyr | Cys |
| 1 | | | | 5 | | | | 10 | | | | | | 15 | |

(2) INFORMATION FOR SEQ ID NO:94:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 16 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:94:

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Leu | Gly | Leu | Gly | Tyr | Ala | Ser | Glu | Glu | Lys | Ile | Ile | Phe | Arg | Tyr | Cys |
| 1 | | | | 5 | | | | 10 | | | | | | 15 | |

(2) INFORMATION FOR SEQ ID NO:95:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 23 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:95:

AGTCGGGGTT GGGGTATGCC TCA

23

(2) INFORMATION FOR SEQ ID NO:96:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 26 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:96:

TATGCCTCAG AGGAGAAGAT TATCTT

26

(2) INFORMATION FOR SEQ ID NO:97:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 336 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:97:

| | |
|---|-----|
| CCTCAGAGGA GAAGATTATC TTCCGATACT GTGCTGGCAG CTGTCCCCAA GAGGTCCGTA | 60 |
| CCCAGCACAG TCTGGTGCTG GCCCGTCTTC GAGGGCAGGG TCGAGCTCAT GGCAGACCTT | 120 |
| GCTGCCAGCC CACCAGCTAT GCTGATGTGA CCTTCCTTGA TGACCACCAC CATTGGCAGC | 180 |
| AGCTGCCTCA GCTCTCAGCC GCAGCTTGTG GCTGTGGTGG CTGAAGGCGG CCAGCCTGGT | 240 |
| CTCTCAGAAT CACAAGCAAG AGGCAGCCTT TGAAAGGCTC AGGTGACGTT ATTAGAAACT | 300 |
| TGCATAGGAG AAGATTAAGA AGAGAAAGGG GACCTG | 336 |

(2) INFORMATION FOR SEQ ID NO:98:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 17 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:98:

Ala Cys Cys Arg Pro Val Ala Phe Asp Asp Asp Leu Ser Phe Leu Asp
 1 5 10 15

Asp

(2) INFORMATION FOR SEQ ID NO:99:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 17 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:99:

Pro Cys Cys Arg Pro Thr Ala Tyr Glu Asp Glu Val Ser Phe Lys Asp
 1 5 10 15

Val

(2) INFORMATION FOR SEQ ID NO:100:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 16 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:100:

Pro Cys Cys Gln Pro Thr Ser Tyr Ala Asp Val Thr Phe Leu Asp Asp
 1 5 10 15

(2) INFORMATION FOR SEQ ID NO:101:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 26 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:101:

TCATCAAGGA AGGTCACATC AGCATA

26

(2) INFORMATION FOR SEQ ID NO:102:

- (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 32 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:102:

CCACCACAGC CACAAGCTGC GGCTGAGAGC TG

32

(2) INFORMATION FOR SEQ ID NO:103:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 5 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:103:

Ala Leu Ala Gly Ser
 1 5

(2) INFORMATION FOR SEQ ID NO:104:

(i) SEQUENCE CHARACTERISTICS:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:104:

This sequence is intentionally skipped

(2) INFORMATION FOR SEQ ID NO:105:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 544 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:105:

| | |
|---|-----|
| GAGGGACCTG GAGCCCCAT CAGGGTAAGA ATTCCTGGGG GCCTCCCGAC TCCCCAATTC | 60 |
| CTTCTCTCAA AGCCCTCACT TTGCCTTACA ATCCTACTCT ACCTTGCACT AGGTAACAAC | 120 |
| CATGTCCGTC TTCCAAGAGC CTTGGCTGGT TCATGCCGAC TGTGGAGCCT GACCCTACCA | 180 |
| GTGGCTGAGC TGGGCCTGGG CTATGCCTCG GAGGAGAAGG TCATCTTCCG ATACTGTGCT | 240 |


```

GGCAGCTGTC CCCAAGAGGC CCGTACCCAG CACAGTCTGG TACTGGCCCG GCTTCGAGGG      300
CGGGGTCGAG CCCATGGCCG ACCCTGCTGC CAGCCCACCA GCTATGCTGA TGTGACCTTC      360
CTTGATGATC AGCACCATTG GCAGCAGCTG CCTCAGCTCT CAGCTGCAGC TTGTGGCTGT      420
GGTGGCTGAA GGAGGCCAGT CTGGTGTCTC AGAATCACAA GCATGAGACA GGCTGGGCTT      480
TGAAAGGCTC AGGTGACATT ACTAGAAATT TGCATAGGTA AAGATAAGAA GGGAAAGGAC      540
CAGG                                                                    544

```

(2) INFORMATION FOR SEQ ID NO:106:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 73 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:106:

```

Ser Glu Glu Lys Ile Ile Phe Arg Tyr Cys Ala Gly Ser Cys Pro Gln
 1             5             10             15
Glu Val Arg Thr Gln His Ser Leu Val Leu Ala Arg Leu Arg Gly Gln
          20             25             30
Gly Arg Ala His Gly Arg Pro Cys Cys Gln Pro Thr Ser Tyr Ala Asp
          35             40             45
Val Thr Phe Leu Asp Asp His His His Trp Gln Gln Leu Pro Gln Leu
          50             55             60
Ser Ala Ala Ala Cys Gly Cys Gly Gly
65             70

```

(2) INFORMATION FOR SEQ ID NO:107:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 391 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:107:

```

TGCCGGCTGT GGAGCCTGAC CCTACCAGTG GCTGAGCTTG GCCTGGGCTA TGCCTCAGAG      60
GAGAAGATTA TCTTCCGATA CTGTGCTGGC AGCTGTCCCC AAGAGGTCCG TACCCAGCAC      120
AGTCTGGTGC TGGCCCGTCT TCGAGGGCAG GGTCGAGCTC ATGGCAGACC TTGCTGCCAG      180
CCCACCAGCT ATGCTGATGT GACCTTCCTT GATGACCACC ACCATTGGCA GCAGCTGCCT      240

```

CAGCTCTCAG CCGCAGCTTG TGGCTGTGGT GGCTGAAGGC GGCCAGCCTG GTCTCTCAGA 300
 ATCACAAGCA AGAGGCAGCC TTTGAAAGGC TCAGGTGACG TTATTAGAAA CTTGCATAGG 360
 AGAAGATTAA GAAGAGAAAG GGGACCTGAT T 391

(2) INFORMATION FOR SEQ ID NO:108:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 8 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (ix) FEATURE:
 - (A) NAME/KEY: Modified-site
 - (B) LOCATION: 2
 - (D) OTHER INFORMATION: /note= "SERINE, THREONINE, OR ALANINE"
- (ix) FEATURE:
 - (A) NAME/KEY: Modified-site
 - (B) LOCATION: 3
 - (D) OTHER INFORMATION: /note= "GLUTAMIC ACID OR ASPARTIC ACID"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:108:

Val Xaa Xaa Leu Gly Leu Gly Tyr
 1 5

(2) INFORMATION FOR SEQ ID NO:109:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 8 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (ix) FEATURE:
 - (A) NAME/KEY: Modified-site
 - (B) LOCATION: 5
 - (D) OTHER INFORMATION: /note= "ALANINE OR SERINE"
- (ix) FEATURE:
 - (A) NAME/KEY: Modified-site
 - (B) LOCATION: 7
 - (D) OTHER INFORMATION: /note= "ALANINE OR SERINE"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:109:

Phe Arg Tyr Cys Xaa Gly Xaa Cys
 1 5

(2) INFORMATION FOR SEQ ID NO:110:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 8 amino acids

(B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(ix) FEATURE:
 (A) NAME/KEY: Modified-site
 (B) LOCATION: 2
 (D) OTHER INFORMATION: /note= "ASPARTIC ACID, GLUTAMIC
 ACID OR NO AMINO ACID"

(ix) FEATURE:
 (A) NAME/KEY: Modified-site
 (B) LOCATION: 3
 (D) OTHER INFORMATION: /note= "VALINE OR LEUCINE"

(ix) FEATURE:
 (A) NAME/KEY: Modified-site
 (B) LOCATION: 4
 (D) OTHER INFORMATION: /note= "SERINE OR THREONINE"

(ix) FEATURE:
 (A) NAME/KEY: Modified-site
 (B) LOCATION: 8
 (D) OTHER INFORMATION: /note= "valine or aspartic acid"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:110:

Asp Xaa Xaa Xaa Phe Leu Asp Xaa
 1 5

(2) INFORMATION FOR SEQ ID NO:111:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 142 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:111:

Glu Gly Pro Gly Arg Pro Ile Arg Val Arg Ile Pro Gly Gly Leu Pro
 1 5 10 15
 Thr Pro Gln Phe Leu Leu Ser Lys Pro Ser Leu Cys Leu Thr Ile Leu
 20 25 30
 Leu Tyr Leu Ala Leu Gly Asn Asn His Val Arg Leu Pro Arg Ala Leu
 35 40 45
 Ala Gly Ser Cys Arg Leu Trp Ser Leu Thr Leu Pro Val Ala Glu Leu
 50 55 60
 Gly Leu Gly Tyr Ala Ser Glu Glu Lys Val Ile Phe Arg Tyr Cys Ala
 65 70 75 80
 Gly Ser Cys Pro Gln Glu Ala Arg Thr Gln His Ser Leu Val Leu Ala
 85 90 95

```

Arg Leu Arg Gly Arg Gly Arg Ala His Gly Arg Pro Cys Cys Gln Pro
    100                                105                                110

Thr Ser Tyr Ala Asp Val Thr Phe Leu Asp Asp Gln His His Trp Gln
    115                                120                                125

Gln Leu Pro Gln Leu Ser Ala Ala Cys Gly Cys Gly Gly
    130                                135                                140

```

(2) INFORMATION FOR SEQ ID NO:112:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 5 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:112:

```

Ala Leu Pro Gly Leu
1          5

```

(2) INFORMATION FOR SEQ ID NO:113:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 12 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 2
- (D) OTHER INFORMATION: /note= "THREONINE, GLUTAMIC ACID OR LYSINE"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 3
- (D) OTHER INFORMATION: /note= "VALINE, LEUCINE OR ISOLEUCINE"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 4
- (D) OTHER INFORMATION: /note= "LEUCINE OR ISOLEUCINE"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 9
- (D) OTHER INFORMATION: /note= "ALANINE OR SERINE"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 11
- (D) OTHER INFORMATION: /note= "ALANINE OR SERINE"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:113:

| | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Glu | Xaa | Xaa | Xaa | Phe | Arg | Tyr | Cys | Xaa | Gly | Xaa | Cys |
| 1 | | | | 5 | | | | | 10 | | |

(2) INFORMATION FOR SEQ ID NO:114:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 16 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

- (ix) FEATURE:
 - (A) NAME/KEY: Modified-site
 - (B) LOCATION: 3
 - (D) OTHER INFORMATION: /note= "ARGININE OR GLUTAMINE"

- (ix) FEATURE:
 - (A) NAME/KEY: Modified-site
 - (B) LOCATION: 5
 - (D) OTHER INFORMATION: /note= "THREONINE, VALINE OR ISOLEUCINE"

- (ix) FEATURE:
 - (A) NAME/KEY: Modified-site
 - (B) LOCATION: 6
 - (D) OTHER INFORMATION: /note= "ALANINE OR SERINE"

- (ix) FEATURE:
 - (A) NAME/KEY: Modified-site
 - (B) LOCATION: 7
 - (D) OTHER INFORMATION: /note= "TYROSINE OR PHENYLALANINE"

- (ix) FEATURE:
 - (A) NAME/KEY: Modified-site
 - (B) LOCATION: 8
 - (D) OTHER INFORMATION: /note= "GLUTAMIC ACID, ASPARTIC ACID OR ALANINE"

- (ix) FEATURE:
 - (A) NAME/KEY: Modified-site
 - (B) LOCATION: 10
 - (D) OTHER INFORMATION: /note= "GLUTAMIC ACID, ASPARTIC ACID OR NO AMINO ACID"

- (ix) FEATURE:
 - (A) NAME/KEY: Modified-site
 - (B) LOCATION: 11
 - (D) OTHER INFORMATION: /note= "VALINE OR LEUCINE"

- (ix) FEATURE:
 - (A) NAME/KEY: Modified-site
 - (B) LOCATION: 12
 - (D) OTHER INFORMATION: /note= "SERINE OR THREONINE"

- (ix) FEATURE:
 - (A) NAME/KEY: Modified-site
 - (B) LOCATION: 16
 - (D) OTHER INFORMATION: /note= "ASPARTIC ACID OR VALINE"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:114:

| | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Cys | Cys | Xaa | Pro | Xaa | Xaa | Xaa | Asp | Xaa | Xaa | Xaa | Phe | Leu | Asp | Xaa |
| 1 | | | | 5 | | | | 10 | | | | | 15 | |

(2) INFORMATION FOR SEQ ID NO:115:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 23 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:115:

GTNDGNGANY TGGGNYTGGG NTA

23

(2) INFORMATION FOR SEQ ID NO:116:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 19 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:116:

GANBTNWCNT TYYTNGANG

19

(2) INFORMATION FOR SEQ ID NO:117:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:117:

GANBTNWCNT TYYTNGANGW

20

(2) INFORMATION FOR SEQ ID NO:118:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 23 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:118:

TTYMGNTAYT GYDSNGGNDG NTG

23

(2) INFORMATION FOR SEQ ID NO:119:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:119:

GTNDGNGANY TGGGNYTNGG

20

(2) INFORMATION FOR SEQ ID NO:120:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 23 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:120:

GTNDGNGANY TGGGNYTGGG NTT

23

(2) INFORMATION FOR SEQ ID NO:121:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:121:

WCNTCNARRA ANGWNAVNTC

20

(2) INFORMATION FOR SEQ ID NO:122:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 19 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:122:

WCNTCNARRA ANGWNAVNT

19

(2) INFORMATION FOR SEQ ID NO:123:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 23 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:123:

CANSHNCCNS HRCARTANCK RAA

23

(2) INFORMATION FOR SEQ ID NO:124:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 25 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:124:

CANSHNCCNS HRCARTANCK RAANA

25

(2) INFORMATION FOR SEQ ID NO:125:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 8 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 2
- (D) OTHER INFORMATION: /note= "THREONINE, SERINE OR ALANINE"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 3
- (D) OTHER INFORMATION: /note= "GLUTAMIC ACID OR ASPARTIC ACID"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:125:

Val Xaa Xaa Leu Gly Leu Gly Tyr
1 5

(2) INFORMATION FOR SEQ ID NO:126:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 7 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(ix) FEATURE:
(A) NAME/KEY: Modified-site
(B) LOCATION: 1
(D) OTHER INFORMATION: /note= "ASPARTIC ACID OR GLUTAMIC
ACID"

(ix) FEATURE:
(A) NAME/KEY: Modified-site
(B) LOCATION: 2
(D) OTHER INFORMATION: /note= "VALINE OR LEUCINE"

(ix) FEATURE:
(A) NAME/KEY: Modified-site
(B) LOCATION: 3
(D) OTHER INFORMATION: /note= "THREONINE OR SERINE"

(ix) FEATURE:
(A) NAME/KEY: Modified-site
(B) LOCATION: 6
(D) OTHER INFORMATION: /note= "ASPARTIC ACID OR GLUTAMIC
ACID"

(ix) FEATURE:
(A) NAME/KEY: Modified-site
(B) LOCATION: 7
(D) OTHER INFORMATION: /note= "ASPARTIC ACID OR VALINE"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:126:

Xaa Xaa Xaa Phe Leu Xaa Xaa
1 5

(2) INFORMATION FOR SEQ ID NO:127:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 8 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(ix) FEATURE:
(A) NAME/KEY: Modified-site
(B) LOCATION: 5
(D) OTHER INFORMATION: /note= "SERINE OR ALANINE"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 7
- (D) OTHER INFORMATION: /note= "SERINE OR ALANINE"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:127:

Phe Arg Tyr Cys Xaa Gly Xaa Cys
1 5

(2) INFORMATION FOR SEQ ID NO:128:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 7 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 2
- (D) OTHER INFORMATION: /note= "THREONINE, SERINE OR ALANINE"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 3
- (D) OTHER INFORMATION: /note= "ASPARTIC ACID OR GLUTAMIC ACID"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:128:

Val Xaa Xaa Leu Gly Leu Gly
1 5

(2) INFORMATION FOR SEQ ID NO:129:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 8 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 2
- (D) OTHER INFORMATION: /note= "THREONINE, SERINE OR ALANINE"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 3
- (D) OTHER INFORMATION: /note= "GLUTAMIC ACID OR ASPARTIC ACID"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:129:

Val Xaa Xaa Leu Gly Leu Gly Phe
 1 5

(2) INFORMATION FOR SEQ ID NO:130:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 9 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (ix) FEATURE:
 - (A) NAME/KEY: Modified-site
 - (B) LOCATION: 1
 - (D) OTHER INFORMATION: /note= "ISOLEUCINE OR LEUCINE"
- (ix) FEATURE:
 - (A) NAME/KEY: Modified-site
 - (B) LOCATION: 6
 - (D) OTHER INFORMATION: /note= "SERINE OR ALANINE"
- (ix) FEATURE:
 - (A) NAME/KEY: Modified-site
 - (B) LOCATION: 8
 - (D) OTHER INFORMATION: /note= "SERINE OR ALANINE"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:130:

Xaa Phe Arg Tyr Cys Xaa Gly Xaa Cys
 1 5

(2) INFORMATION FOR SEQ ID NO:131:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 559 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:131:

| | |
|--|-----|
| ATGGCTGCAG GAAGACTTCG GATCCTGTGT CTGCTGCTCC TGTCTTGCA CCCGAGCCTC | 60 |
| GGCTGGGTCC TTGATCTTCA AGAGGCTTCT GTGGCAGATA AGCTCTCATT TGGGAAGATG | 120 |
| GCAGAGACTA GAGGGACCTG GACGCCCCAT CAGGGTAAGA ATTCCTGGGG GCCTCCCGAC | 180 |
| TCCCCAATTC CTTCTCTCAA AGCCCTCACT TTGCCTTACA ATCCTACTCT ACCTTGCACT | 240 |
| AGGTAACAAC CATGTCCGTC TTCCAAGAGC CTTGGCTGGT TCATGCCGAC TGTGGAGCCT | 300 |
| GACCCTACCA GTGGCTGAGC TGGGCCTGGG CTATGCCTCG GAGGAGAAGG TCATCTTCCG | 360 |
| ATACTGTGCT GGCAGCTGTC CCCAAGAGGC CCGTACCCAG CACAGTCTGG TACTGGCCCCG | 420 |
| GCTTCGAGGG CGGGGTCGAG CCCATGGCCG ACCCTGCTGC CAGCCCACCA GCTATGCTGA | 480 |

TGTGACCTTC CTTGATGATC AGCACCATTG GCAGCAGCTG CCTCAGCTCT CAGCTGCAGC 540
 TTGTGGCTGT GGTGGCTGA 559

(2) INFORMATION FOR SEQ ID NO:132:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 133 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:132:

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Pro | Asp | Ala | Arg | Gly | Val | Pro | Val | Ala | Asp | Gly | Glu | Phe | Ser | Ser | Glu |
| 1 | | | | 5 | | | | | 10 | | | | | 15 | |
| Gln | Val | Ala | Lys | Ala | Gly | Gly | Thr | Trp | Leu | Gly | Thr | His | Arg | Pro | Leu |
| | | | 20 | | | | | 25 | | | | | 30 | | |
| Ala | Arg | Leu | Arg | Arg | Ala | Leu | Ser | Gly | Pro | Cys | Gln | Leu | Trp | Ser | Leu |
| | | 35 | | | | | 40 | | | | | 45 | | | |
| Thr | Leu | Ser | Val | Ala | Glu | Leu | Gly | Leu | Gly | Tyr | Ala | Ser | Glu | Glu | Lys |
| | 50 | | | | | 55 | | | | | 60 | | | | |
| Val | Ile | Phe | Arg | Tyr | Cys | Ala | Gly | Ser | Cys | Pro | Arg | Gly | Ala | Arg | Thr |
| 65 | | | | | 70 | | | | | 75 | | | | 80 | |
| Gln | His | Gly | Leu | Ala | Leu | Ala | Arg | Leu | Gln | Gly | Gln | Gly | Arg | Ala | His |
| | | | 85 | | | | | | 90 | | | | | 95 | |
| Gly | Gly | Pro | Cys | Cys | Arg | Pro | Thr | Arg | Tyr | Thr | Asp | Val | Ala | Phe | Leu |
| | | | 100 | | | | | 105 | | | | | 110 | | |
| Asp | Asp | Arg | His | Arg | Trp | Gln | Arg | Leu | Pro | Gln | Leu | Ser | Ala | Ala | Ala |
| | | 115 | | | | | 120 | | | | | 125 | | | |
| Cys | Gly | Cys | Gly | Gly | | | | | | | | | | | |
| | | | 130 | | | | | | | | | | | | |

(2) INFORMATION FOR SEQ ID NO:133:

- (i) SEQUENCE CHARACTERISTICS:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:133:

This sequence is intentionally skipped

(2) INFORMATION FOR SEQ ID NO:134:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 93 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:134:

```

Cys Val Leu Thr Ala Ile His Leu Asn Val Thr Asp Leu Gly Leu Gly
1           5           10           15
Tyr Glu Thr Lys Glu Glu Leu Ile Phe Arg Tyr Cys Ser Gly Ser Cys
20           25           30
Glu Ala Ala Glu Thr Met Tyr Asp Lys Ile Leu Lys Asn Leu Ser Arg
35           40           45
Ser Arg Arg Leu Thr Ser Asp Lys Val Gly Gln Ala Cys Cys Arg Pro
50           55           60
Val Ala Phe Asp Asp Asp Leu Ser Phe Leu Asp Asp Ser Leu Val Tyr
65           70           75           80
His Ile Leu Arg Lys His Ser Ala Lys Arg Cys Gly Cys
85           90

```

(2) INFORMATION FOR SEQ ID NO:135:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 23 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:135:

```

Met Ala Ala Gly Arg Leu Arg Ile Leu Cys Leu Leu Leu Leu Ser Leu
1           5           10           15
His Pro Ser Leu Gly Trp Val
20

```

(2) INFORMATION FOR SEQ ID NO:136:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 23 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:136:

```

Met Ala Ala Gly Arg Leu Arg Ile Leu Phe Leu Leu Leu Leu Ser Leu
1           5           10           15
His Leu Gly Leu Gly Trp Val
20

```

(2) INFORMATION FOR SEQ ID NO:137:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 23 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:137:

AATCCCCAGG ACAGGCAGGG AAT

23

(2) INFORMATION FOR SEQ ID NO:138:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 35 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:138:

CGGTACCCAG ATCTTCAGCC ACCACAGCCA CAAGC

35

(2) INFORMATION FOR SEQ ID NO:139:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 76 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:139:

GGACTATCAT ATGGCCCACC ACCACCACCA CCACCACCAC GACGACGACG ACAAGGCCTT
GGCTGGTTCA TGCCGA

60

76

(2) INFORMATION FOR SEQ ID NO:140:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 32 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:140:

TGCTGTCACC ATGGCTGCAG GAAGACTTCG GA

32

(2) INFORMATION FOR SEQ ID NO:141:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 96 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:141:

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Ala | Leu | Ala | Gly | Ser | Cys | Arg | Leu | Trp | Ser | Leu | Thr | Leu | Pro | Val | Ala |
| 1 | | | | 5 | | | | | 10 | | | | | 15 | |
| Glu | Leu | Gly | Leu | Gly | Tyr | Ala | Ser | Glu | Glu | Lys | Val | Ile | Phe | Arg | Tyr |
| | | | 20 | | | | | 25 | | | | | 30 | | |
| Cys | Ala | Gly | Ser | Cys | Pro | Gln | Glu | Ala | Arg | Thr | Gln | His | Ser | Leu | Val |
| | | 35 | | | | | 40 | | | | | 45 | | | |
| Leu | Ala | Arg | Leu | Arg | Gly | Arg | Gly | Arg | Ala | His | Gly | Arg | Pro | Cys | Cys |
| | 50 | | | | 55 | | | | | | 60 | | | | |
| Arg | Pro | Thr | Ala | Tyr | Glu | Asp | Glu | Val | Ser | Phe | Leu | Asp | Val | His | Ser |
| 65 | | | | 70 | | | | | 75 | | | | | 80 | |
| Arg | Tyr | His | Thr | Leu | Gln | Glu | Leu | Ser | Ala | Arg | Glu | Cys | Ala | Cys | Val |
| | | | 85 | | | | | 90 | | | | | | 95 | |

(2) INFORMATION FOR SEQ ID NO:142:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 23 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:142:

TAATACGACT CACTATAGGG GAA

23

(2) INFORMATION FOR SEQ ID NO:143:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 49 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:143:

TCGTCTTCGT AAGCAGTCGG ACGGCAGCAG GGTCGGCCAT GGGCTCGAC

49

(2) INFORMATION FOR SEQ ID NO:144:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 29 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:144:

TGCTGCCGTC CGACTGCTTA CGAAGACGA

29

(2) INFORMATION FOR SEQ ID NO:145:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 25 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:145:

GTTATGCTAG TTATTGCTCA GCGGT

25

(2) INFORMATION FOR SEQ ID NO:146:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 100 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:146:

Pro Gly Ala Arg Pro Cys Gly Leu Arg Glu Leu Glu Val Arg Val Ser
1 5 10 15

Glu Leu Gly Leu Gly Tyr Thr Ser Asp Glu Thr Val Leu Phe Arg Tyr
20 25 30

Cys Ala Gly Ala Cys Glu Ala Ala Ile Arg Ile Tyr Asp Leu Gly Leu
35 40 45

Arg Arg Leu Arg Gln Arg Arg Arg Val Arg Arg Glu Arg Ala Arg Ala
50 55 60

His Pro Cys Cys Gln Pro Thr Ser Tyr Ala Asp Val Thr Phe Leu Asp
65 70 75 80

Asp Gln His His Trp Gln Gln Leu Pro Gln Leu Ser Ala Ala Ala Cys
85 90 95

Gly Cys Gly Gly
100

(2) INFORMATION FOR SEQ ID NO:147:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 50 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:147:

CACATCAGCA TAGCTGGTGG GCTGGCAGCA CGGGTGAGCA CGAGCACGTT 50

(2) INFORMATION FOR SEQ ID NO:148:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 25 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:148:

TGCTGCCAGC CCACCAGCTA TGCTG 25

(2) INFORMATION FOR SEQ ID NO:149:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 23 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:149:

CCTCGGAGGA GAAGTCATC TTC 23

(2) INFORMATION FOR SEQ ID NO:150:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 98 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:150:

```

Cys Cys Val Arg Gln Leu Tyr Ile Asp Phe Arg Lys Asp Leu Gly Trp
1          5          10          15
Lys Trp Ile His Glu Pro Lys Gly Tyr His Ala Asn Phe Cys Leu Gly
          20          25          30
Pro Cys Pro Tyr Ile Trp Ser Leu Asp Thr Gln Tyr Ser Lys Val Leu
          35          40          45
Ala Leu Tyr Asn Gln His Asn Pro Gly Ala Ser Ala Ala Pro Cys Cys
          50          55          60
Val Pro Gln Ala Leu Glu Pro Leu Pro Ile Val Tyr Tyr Val Gly Arg
          65          70          75          80
Lys Pro Lys Val Glu Gln Leu Ser Asn Met Ile Val Arg Ser Cys Lys
          85          90          95
Cys Ser

```

(2) INFORMATION FOR SEQ ID NO:151:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 98 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:151:

```

Cys Cys Leu Arg Pro Leu Tyr Ile Asp Phe Lys Arg Asp Leu Gly Trp
1          5          10          15
Lys Trp Ile His Glu Pro Lys Gly Tyr Asn Ala Asn Phe Cys Ala Gly
          20          25          30
Ala Cys Pro Tyr Leu Trp Ser Ser Asp Thr Gln His Ser Arg Val Leu
          35          40          45
Ser Leu Tyr Asn Thr Ile Asn Pro Glu Ala Ser Ala Ser Pro Cys Cys
          50          55          60
Val Ser Gln Asp Leu Glu Pro Leu Thr Ile Leu Tyr Tyr Ile Gly Lys
          65          70          75          80
Thr Pro Lys Ile Glu Gln Leu Ser Asn Met Ile Val Lys Ser Cys Lys
          85          90          95
Cys Ser

```

(2) INFORMATION FOR SEQ ID NO:152:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 98 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:152:

```

Cys Cys Val Arg Pro Leu Tyr Ile Asp Phe Arg Gln Asp Leu Gly Trp
1          5          10          15
Lys Trp Val His Glu Pro Lys Gly Tyr Tyr Ala Asn Phe Cys Ser Gly
          20          25          30
Pro Cys Pro Tyr Leu Arg Ser Ala Asp Thr Thr His Ser Thr Val Leu
          35          40          45
Gly Leu Tyr Asn Thr Leu Asn Pro Glu Ala Ser Ala Ser Pro Cys Cys
          50          55          60
Val Pro Gln Asp Leu Glu Pro Leu Thr Ile Leu Tyr Tyr Val Gly Arg
          65          70          75          80
Thr Pro Lys Val Glu Gln Leu Ser Asn Met Val Val Lys Ser Cys Lys
          85          90          95
Cys Ser

```

(2) INFORMATION FOR SEQ ID NO:153:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 106 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:153:

```

Cys Cys Lys Lys Gln Phe Phe Val Ser Phe Lys Asp Ile Gly Trp Asn
1          5          10          15
Asp Trp Ile Ile Ala Pro Ser Gly Tyr His Ala Asn Tyr Cys Glu Gly
          20          25          30
Glu Cys Pro Ser His Ile Ala Gly Thr Ser Gly Ser Ser Leu Ser Phe
          35          40          45
His Ser Thr Val Ile Asn His Tyr Arg Met Arg Gly His Ser Pro Phe
          50          55          60
Ala Asn Leu Lys Ser Cys Cys Val Pro Thr Lys Leu Arg Pro Met Ser
          65          70          75          80

```

Met Leu Tyr Tyr Asp Asp Gly Gln Asn Ile Ile Lys Lys Asp Ile Gln
 85 90 95

Asn Met Ile Val Glu Glu Cys Gly Cys Ser
 100 105

(2) INFORMATION FOR SEQ ID NO:154:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 105 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:154:

Cys Cys Arg Gln Gln Phe Phe Ile Asp Phe Arg Leu Ile Gly Trp Asn
 1 5 10 15

Asp Trp Ile Ile Ala Pro Thr Gly Tyr Tyr Gly Asn Tyr Cys Glu Gly
 20 25 30

Ser Cys Pro Ala Tyr Leu Ala Gly Val Pro Gly Ser Ala Ser Ser Phe
 35 40 45

His Thr Ala Val Val Asn Gln Tyr Arg Met Arg Gly Leu Asn Pro Gly
 50 55 60

Thr Val Asn Ser Cys Cys Ile Pro Thr Lys Leu Ser Thr Met Ser Met
 65 70 75 80

Leu Tyr Phe Asp Asp Glu Tyr Asn Ile Val Lys Arg Asp Val Pro Asn
 85 90 95

Met Ile Val Glu Glu Cys Gly Cys Ala
 100 105

(2) INFORMATION FOR SEQ ID NO:155:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 101 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:155:

Cys Arg Arg Val Lys Phe Gln Val Asp Phe Asn Leu Ile Gly Trp Gly
 1 5 10 15

Ser Trp Ile Ile Tyr Pro Lys Gln Tyr Asn Ala Tyr Arg Cys Glu Gly
 20 25 30

Glu Cys Pro Asn Pro Val Gly Glu Glu Phe His Pro Thr Asn His Ala
 35 40 45

Tyr Ile Gln Ser Leu Leu Lys Arg Tyr Gln Pro His Arg Val Pro Ser
 50 55 60
 Thr Cys Cys Ala Pro Val Lys Thr Lys Pro Leu Ser Met Leu Tyr Val
 65 70 75 80
 Asp Asn Gly Arg Val Leu Leu Glu His His Lys Asp Met Ile Val Glu
 85 90 95
 Glu Cys Gly Cys Leu
 100

(2) INFORMATION FOR SEQ ID NO:156:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 101 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:156:

Cys Lys Arg His Pro Leu Tyr Val Asp Phe Ser Asp Val Gly Trp Asn
 1 5 10 15
 Asp Trp Ile Val Ala Pro Pro Gly Tyr His Ala Phe Tyr Cys His Gly
 20 25 30
 Glu Cys Pro Phe Pro Leu Ala Asp His Leu Asn Ser Thr Asn His Ala
 35 40 45
 Ile Val Gln Thr Leu Val Asn Ser Val Asn Ser Lys Ile Pro Lys Ala
 50 55 60
 Cys Cys Val Pro Thr Glu Leu Ser Ala Ile Ser Met Leu Tyr Leu Asp
 65 70 75 80
 Glu Asn Glu Lys Val Val Leu Lys Asn Tyr Gln Asp Met Val Val Glu
 85 90 95
 Gly Cys Gly Cys Arg
 100

(2) INFORMATION FOR SEQ ID NO:157:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 101 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:157:

Cys Arg Arg His Ser Leu Tyr Val Asp Phe Ser Asp Val Gly Trp Asn
 1 5 10 15

```

Asp Trp Ile Val Ala Pro Pro Gly Tyr Gln Ala Phe Tyr Cys His Gly
      20                      25                      30
Asp Cys Pro Phe Pro Leu Ala Asp His Leu Asn Ser Thr Asn His Ala
      35                      40                      45
Ile Val Gln Thr Leu Val Asn Ser Val Asn Ser Ser Ile Pro Lys Ala
      50                      55                      60
Cys Cys Val Pro Thr Glu Leu Ser Ala Ile Ser Met Leu Tyr Leu Asp
      65                      70                      75                      80
Glu Tyr Asp Lys Val Val Leu Lys Asn Tyr Gln Glu Met Val Val Glu
      85                      90                      95
Gly Cys Gly Cys Arg
      100

```

(2) INFORMATION FOR SEQ ID NO:158:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 102 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:158:

```

Cys Arg Arg His Ser Leu Tyr Val Asp Phe Ser Asp Val Gly Trp Asp
1          5          10          15
Asp Trp Ile Val Ala Pro Leu Gly Tyr Asp Ala Tyr Tyr Cys His Gly
      20                      25                      30
Lys Cys Pro Phe Pro Leu Ala Asp His Phe Asn Ser Thr Asn His Ala
      35                      40                      45
Val Val Gln Thr Leu Val Asn Asn Met Asn Pro Gly Lys Val Pro Lys
      50                      55                      60
Ala Cys Cys Val Pro Thr Gln Leu Asp Ser Val Ala Met Leu Tyr Leu
      65                      70                      75                      80
Asn Asp Gln Ser Thr Val Val Leu Lys Asn Tyr Gln Glu Met Thr Val
      85                      90                      95
Val Gly Cys Gly Cys Arg
      100

```

(2) INFORMATION FOR SEQ ID NO:159:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 102 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:159:

Cys Lys Lys His Glu Leu Tyr Val Ser Phe Arg Asp Leu Gly Trp Gln
 1 5 10 15
 Asp Trp Ile Ile Ala Pro Glu Gly Tyr Ala Ala Phe Tyr Cys Asp Gly
 20 25 30
 Glu Cys Ser Phe Pro Leu Asn Ala His Met Asn Ala Thr Asn His Ala
 35 40 45
 Ile Val Gln Thr Leu Val His Leu Met Phe Pro Asp His Val Pro Lys
 50 55 60
 Pro Cys Cys Ala Pro Thr Lys Leu Asn Ala Ile Ser Val Leu Tyr Phe
 65 70 75 80
 Asp Asp Ser Ser Asn Val Ile Leu Lys Lys Tyr Arg Asn Met Val Val
 85 90 95
 Arg Ser Cys Gly Cys His
 100

(2) INFORMATION FOR SEQ ID NO:160:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 102 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:160:

Cys Arg Lys His Glu Leu Tyr Val Ser Phe Gln Asp Leu Gly Trp Gln
 1 5 10 15
 Asp Trp Ile Ile Ala Pro Lys Gly Tyr Ala Ala Asn Tyr Cys Asp Gly
 20 25 30
 Glu Cys Ser Phe Pro Leu Asn Ala His Met Asn Ala Thr Asn His Ala
 35 40 45
 Ile Val Gln Thr Leu Val His Leu Met Asn Pro Glu Tyr Val Pro Lys
 50 55 60
 Pro Cys Cys Ala Pro Thr Lys Leu Asn Ala Ile Ser Val Leu Tyr Phe
 65 70 75 80
 Asp Asp Asn Ser Asn Val Ile Leu Lys Lys Tyr Arg Asn Met Val Val
 85 90 95
 Arg Ala Cys Gly Cys His
 100

(2) INFORMATION FOR SEQ ID NO:161:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 102 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:161:

```

Cys Lys Lys His Glu Leu Tyr Val Ser Phe Arg Asp Leu Gly Trp Gln
 1             5             10             15
Asp Trp Ile Ile Ala Pro Glu Gly Tyr Ala Ala Tyr Tyr Cys Glu Gly
          20             25             30
Glu Cys Ala Phe Pro Leu Asn Ser Tyr Met Asn Ala Thr Asn His Ala
          35             40             45
Ile Val Gln Thr Leu Val His Phe Ile Asn Pro Glu Thr Val Pro Lys
          50             55             60
Pro Cys Cys Ala Pro Thr Gln Leu Asn Ala Ile Ser Val Leu Tyr Phe
          65             70             75             80
Asp Asp Ser Ser Asn Val Ile Leu Lys Lys Tyr Arg Asn Met Val Val
          85             90             95
Arg Ala Cys Gly Cys His
          100

```

(2) INFORMATION FOR SEQ ID NO:162:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 102 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:162:

```

Cys Arg Arg His Glu Leu Tyr Val Ser Phe Gln Asp Leu Gly Trp Leu
 1             5             10             15
Asp Trp Val Ile Ala Pro Gln Gly Tyr Ser Ala Tyr Tyr Cys Glu Gly
          20             25             30
Glu Cys Ser Phe Pro Leu Asp Ser Cys Met Asn Ala Thr Asn His Ala
          35             40             45
Ile Leu Gln Ser Leu Val His Leu Met Lys Pro Asn Ala Val Pro Lys
          50             55             60
Ala Cys Cys Ala Pro Thr Lys Leu Ser Ala Thr Ser Val Leu Tyr Tyr
          65             70             75             80
Asp Ser Ser Asn Asn Val Ile Leu Arg Lys His Arg Asn Met Val Val
          85             90             95
Lys Ala Cys Gly Cys His
          100

```


(2) INFORMATION FOR SEQ ID NO:163:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 102 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:163:

```

Cys Gln Met Gln Thr Leu Tyr Ile Asp Phe Lys Asp Leu Gly Trp His
1      5      10      15
Asp Trp Ile Ile Ala Pro Glu Gly Tyr Gly Ala Phe Tyr Cys Ser Gly
20     25     30
Glu Cys Asn Phe Pro Leu Asn Ala His Met Asn Ala Thr Asn His Ala
35     40     45
Ile Val Gln Thr Leu Val His Leu Leu Glu Pro Lys Lys Val Pro Lys
50     55     60
Pro Cys Cys Ala Pro Thr Arg Leu Gly Ala Leu Pro Val Leu Tyr His
65     70     75     80
Leu Asn Asp Glu Asn Val Asn Leu Lys Lys Tyr Arg Asn Met Ile Val
85     90     95
Lys Ser Cys Gly Cys His
100

```

(2) INFORMATION FOR SEQ ID NO:164:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 103 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:164:

```

Cys Ala Arg Arg Tyr Leu Lys Val Asp Phe Ala Asp Ile Gly Trp Ser
1      5      10      15
Glu Trp Ile Ile Ser Pro Lys Ser Phe Asp Ala Tyr Tyr Cys Ser Gly
20     25     30
Ala Cys Gln Phe Pro Met Pro Lys Ser Leu Lys Pro Ser Asn His Ala
35     40     45
Thr Ile Gln Ser Ile Val Arg Ala Val Gly Val Val Pro Gly Ile Pro
50     55     60
Glu Pro Cys Cys Val Pro Glu Lys Met Ser Ser Leu Ser Ile Leu Phe
65     70     75     80

```

Phe Asp Glu Asn Lys Asn Val Val Leu Lys Val Tyr Pro Asn Met Thr
 85 90 95

Val Glu Ser Cys Ala Cys Arg
 100

(2) INFORMATION FOR SEQ ID NO:165:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 102 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:165:

Cys Lys Lys Arg His Leu Tyr Val Glu Phe Lys Asp Val Gly Trp Gln
 1 5 10 15

Asn Trp Val Ile Ala Pro Gln Gly Tyr Met Ala Asn Tyr Cys Tyr Gly
 20 25 30

Glu Cys Pro Tyr Pro Leu Thr Glu Ile Leu Asn Gly Ser Asn His Ala
 35 40 45

Ile Leu Gln Thr Leu Val His Ser Ile Glu Pro Glu Asp Ile Pro Leu
 50 55 60

Pro Cys Cys Val Pro Thr Lys Met Ser Pro Ile Ser Met Leu Phe Tyr
 65 70 75 80

Asp Asn Asn Asp Asn Val Val Leu Arg His Tyr Glu Asn Met Ala Val
 85 90 95

Asp Glu Cys Gly Cys Arg
 100

(2) INFORMATION FOR SEQ ID NO:166:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 106 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:166:

Cys Arg Ala Arg Arg Leu Tyr Val Ser Phe Arg Glu Val Gly Trp His
 1 5 10 15

Arg Trp Val Ile Ala Pro Arg Gly Phe Leu Ala Asn Tyr Cys Gln Gly
 20 25 30

Gln Cys Ala Leu Pro Val Ala Leu Ser Gly Ser Gly Gly Pro Pro Ala
 35 40 45

Leu Asn His Ala Val Leu Arg Ala Leu Met His Ala Ala Ala Pro Gly
 50 55 60
 Ala Ala Asp Leu Pro Cys Cys Val Pro Ala Arg Leu Ser Pro Ile Ser
 65 70 75 80
 Val Leu Phe Phe Asp Asn Ser Asp Asn Val Val Leu Arg Gln Tyr Glu
 85 90 95
 Asp Met Val Val Asp Glu Cys Gly Cys Arg
 100 105

(2) INFORMATION FOR SEQ ID NO:167:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 101 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:167:

Cys His Arg His Gln Leu Phe Ile Asn Phe Gln Asp Leu Gly Trp His
 1 5 10 15
 Lys Trp Val Ile Ala Pro Lys Gly Phe Met Ala Asn Tyr Cys His Gly
 20 25 30
 Glu Cys Pro Phe Ser Met Thr Thr Tyr Leu Asn Ser Ser Asn Tyr Ala
 35 40 45
 Phe Met Gln Ala Leu Met His Met Ala Asp Pro Lys Val Pro Lys Ala
 50 55 60
 Val Cys Val Pro Thr Lys Leu Ser Pro Ile Ser Met Leu Tyr Gln Asp
 65 70 75 80
 Ser Asp Lys Asn Val Ile Leu Arg His Tyr Glu Asp Met Val Val Asp
 85 90 95
 Glu Cys Gly Cys Gly
 100

(2) INFORMATION FOR SEQ ID NO:168:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 103 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:168:

Cys Arg Arg Thr Ser Leu His Val Asn Phe Lys Glu Ile Gly Trp Asp
 1 5 10 15

```

Ser Trp Ile Ile Ala Pro Lys Asp Tyr Glu Ala Phe Glu Cys Lys Gly
      20              25              30
Gly Cys Phe Phe Pro Leu Thr Asp Asn Val Thr Pro Thr Lys His Ala
      35              40              45
Ile Val Gln Thr Leu Val His Leu Gln Asn Pro Lys Lys Ala Ser Lys
      50              55              60
Ala Cys Cys Val Pro Thr Lys Leu Asp Ala Ile Ser Ile Leu Tyr Lys
      65              70              75              80
Asp Asp Ala Gly Val Pro Thr Leu Ile Tyr Asn Tyr Glu Gly Met Lys
      85              90              95
Val Ala Glu Cys Gly Cys Arg
      100

```

(2) INFORMATION FOR SEQ ID NO:169:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 105 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:169:

```

Cys His Arg Val Ala Leu Asn Ile Ser Phe Gln Glu Leu Gly Trp Glu
1              5              10              15
Arg Trp Ile Val Tyr Pro Pro Ser Phe Ile Phe His Tyr Cys His Gly
      20              25              30
Gly Cys Gly Leu His Ile Pro Pro Asn Leu Ser Leu Pro Val Pro Gly
      35              40              45
Ala Pro Pro Thr Pro Ala Gln Pro Tyr Ser Leu Leu Pro Gly Ala Gln
      50              55              60
Pro Cys Cys Ala Ala Leu Pro Gly Thr Met Arg Pro Leu His Val Arg
      65              70              75              80
Thr Thr Ser Asp Gly Gly Tyr Ser Phe Lys Tyr Glu Thr Val Pro Asn
      85              90              95
Leu Leu Thr Gln His Cys Ala Cys Ile
      100              105

```

(2) INFORMATION FOR SEQ ID NO:170:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 99 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:170:

Cys Ala Leu Arg Glu Leu Ser Val Asp Leu Arg Ala Glu Arg Ser Val
 1 5 10 15
 Leu Ile Pro Glu Thr Tyr Gln Ala Asn Asn Cys Gln Gly Ala Cys Gly
 20 25 30
 Trp Pro Gln Ser Asp Arg Asn Pro Arg Tyr Gly Asn His Val Val Leu
 35 40 45
 Leu Leu Lys Met Gln Ala Arg Gly Ala Thr Leu Ala Arg Pro Pro Cys
 50 55 60
 Cys Val Pro Thr Ala Tyr Thr Gly Lys Leu Leu Ile Ser Leu Ser Glu
 65 70 75 80
 Glu Arg Ile Ser Ala His His Val Pro Asn Met Val Ala Thr Glu Cys
 85 90 95
 Gly Cys Arg

(2) INFORMATION FOR SEQ ID NO:171:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 102 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:171:

Cys Glu Leu His Asp Phe Ser Leu Ser Phe Ser Gln Leu Lys Trp Asp
 1 5 10 15
 Asn Trp Ile Val Ala Pro His Ser Tyr Asn Pro Ser Tyr Cys Lys Gly
 20 25 30
 Asp Cys Pro Ser Ala Val Ser His Arg Tyr Gly Ser Pro Val His Thr
 35 40 45
 Met Val Gln Asn Met Ile Tyr Glu Lys Leu Asp Pro Ser Val Pro Ser
 50 55 60
 Pro Ser Cys Val Pro Gly Lys Tyr Ser Pro Leu Ser Val Leu Thr Ile
 65 70 75 80
 Glu Pro Asp Gly Ser Ile Ala Tyr Lys Glu Tyr Glu Asp Met Met Ala
 85 90 95
 Thr Ser Cys Thr Cys Arg
 100

(2) INFORMATION FOR SEQ ID NO:172:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 94 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:172:

```

Cys Val Leu Thr Ala Ile His Leu Asn Val Thr Asp Leu Gly Leu Gly
 1           5           10           15
Tyr Glu Thr Lys Glu Glu Leu Ile Phe Arg Tyr Cys Ser Gly Ser Cys
      20           25           30
Asp Ala Ala Glu Thr Thr Tyr Asp Lys Ile Leu Lys Asn Leu Ser Arg
      35           40           45
Asn Arg Arg Leu Val Ser Asp Lys Val Gly Gln Ala Cys Cys Arg Pro
      50           55           60
Ile Ala Phe Asp Asp Asp Leu Ser Phe Leu Asp Asp Asn Leu Val Tyr
      65           70           75           80
His Ile Leu Arg Lys His Ser Ala Lys Arg Cys Gly Cys Ile
      85           90

```

(2) INFORMATION FOR SEQ ID NO:173:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 95 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:173:

```

Cys Gly Leu Arg Glu Leu Glu Val Arg Val Ser Glu Leu Gly Leu Gly
 1           5           10           15
Tyr Ala Ser Asp Glu Thr Val Leu Phe Arg Tyr Cys Ala Gly Ala Cys
      20           25           30
Glu Ala Ala Ala Arg Val Tyr Asp Leu Gly Leu Arg Arg Leu Arg Gln
      35           40           45
Arg Arg Arg Leu Arg Arg Glu Arg Val Arg Ala Gln Pro Cys Cys Arg
      50           55           60
Pro Thr Ala Tyr Glu Asp Glu Val Ser Phe Leu Asp Ala His Ser Arg
      65           70           75           80
Tyr His Thr Val His Glu Leu Ser Ala Arg Glu Cys Ala Cys Val
      85           90           95

```

(2) INFORMATION FOR SEQ ID NO:174:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 37 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:174:

```

Leu Asp Leu Gln Glu Ala Ser Val Ala Asp Lys Leu Ser Phe Gly Lys
1           5           10           15
Met Ala Glu Thr Arg Gly Thr Trp Thr Pro His Gln Gly Asn Asn His
20           25           30
Val Arg Leu Pro Arg
35

```

(2) INFORMATION FOR SEQ ID NO:175:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 37 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:175:

```

Leu Asp Leu Gln Glu Ala Pro Ala Ala Asp Glu Leu Ser Ser Gly Lys
1           5           10           15
Met Ala Glu Thr Gly Arg Thr Trp Lys Pro His Gln Gly Asn Asn Asn
20           25           30
Val Arg Leu Pro Arg
35

```

(2) INFORMATION FOR SEQ ID NO:176:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 93 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:176:

```

Cys Val Leu Thr Ala Ile His Leu Asn Val Thr Asp Leu Gly Leu Gly
1           5           10           15
Tyr Glu Thr Lys Glu Glu Leu Ile Phe Arg Tyr Cys Ser Gly Ser Cys
20           25           30
Glu Ser Ala Glu Thr Met Tyr Asp Lys Ile Leu Lys Asn Leu Ser Arg
35           40           45

```

Ser Arg Arg Leu Thr Ser Asp Lys Val Gly Gln Ala Cys Cys Arg Pro
 50 55 60

Val Ala Phe Asp Asp Asp Leu Ser Phe Leu Asp Asp Asn Leu Val Tyr
 65 70 75 80

His Ile Leu Arg Lys His Ser Ala Lys Arg Cys Gly Cys
 85 90

(2) INFORMATION FOR SEQ ID NO:177:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 723 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:177:

| | |
|--|-----|
| ATGGCTGCAG GAAGACTTCG GATCCTGTGT CTGCTGCTCC TGTCTTGCA CCCGAGCCTC | 60 |
| GGCTGGGTCC TTGATCTTCA AGAGGCTTCT GTGCAGATA AGCTCTCATT TGGGAAGATG | 120 |
| GCAGAGACTA GAGGGACCTG GACGCCCCAT CAGGGTAAGA ATTCCTGGGG GCCTCCCGAC | 180 |
| TCCCCAATTC CTTCTCTCAA AGCCCTCACT TTGCCTTACA ATCCTACTCT ACCTTGCACT | 240 |
| AGGTAACAAC CATGTCCGTC TTCCAAGAGC CTTGGCTGGT TCATGCCGAC TGTGGAGCCT | 300 |
| GACCCTACCA GTGGCTGAGC TGGGCCTGGG CTATGCCTCG GAGGAGAAGG TCATCTTCCG | 360 |
| ATACTGTGCT GGCAGCTGTC CCCAAGAGGC CCGTACCCAG CACAGTCTGG TACTGGCCCCG | 420 |
| GCTTCGAGGG CGGGGTCGAG CCCATGGCCG ACCCTGCTGC CAGCCCACCA GCTATGCTGA | 480 |
| TGTGACCTTC CTTGATGATC AGCACCATTG GCAGCAGCTG CCTCAGCTCT CAGCTGCAGC | 540 |
| TTGTGGCTGT GGTGGCTGAA GGAGGCCAGT CTGGTGTCTC AGAATCACAA GCATGAGACA | 600 |
| GGCTGGGCTT TGAAAGGCTC AGGTGACATT ACTAGAAATT TGCATAGGTA AAGATAAGAA | 660 |
| GGGAAAGGAC CAGGGGTTTT TTGTTTCTTT CTTTGCTTGC TTGTTAGTTT TTTTTTTTTT | 720 |
| TTT | 723 |

(2) INFORMATION FOR SEQ ID NO:178:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 723 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:178:

| | |
|--|----|
| AAAAAAAAA AAAAACTAA CAAGCAAGCA AAGAAAGAAA CAAAAAACC CTGGTCCTTT | 60 |
|--|----|


```

CCCTTCTTAT CTTTACCTAT GCAAATTTCT AGTAATGTCA CCTGAGCCTT TCAAAGCCCA      120
GCCTGTCTCA TGCTTGTGAT TCTGAGACAC CAGACTGGCC TCCTTCAGCC ACCACAGCCA      180
CAAGCTGCAG CTGAGAGCTG AGGCAGCTGC TGCCAATGGT GCTGATCATC AAGGAAGGTC      240
ACATCAGCAT AGCTGGTGGG CTGGCAGCAG GGTGCGCCAT GGGCTCGACC CCGCCCTCGA      300
AGCCGGGCCA GTACCAGACT GTGCTGGGTA CGGGCCTCTT GGGGACAGCT GCCAGCACAG      360
TATCGGAAGA TGACCTTCTC CTCCGAGGCA TAGCCAGGC CCAGCTCAGC CACTGGTAGG      420
GTCAGGCTCC ACAGTCGGCA TGAACCAGCC AAGGCTCTTG GAAGACGGAC ATGGTTGTTA      480
CCTAGTGCAA GGTAGAGTAG GATTGTAAGG CAAAGTGAGG GCTTTGAGAG AAGGAATTGG      540
GGAGTCGGGA GGCCCCCAGG AATTCTTACC CTGATGGGGC GTCCAGGTCC CTCTAGTCTC      600
TGCCATCTTC CCAAATGAGA GCTTATCTGC CACAGAAGCC TCTTGAAGAT CAAGGACCCA      660
GCCGAGGCTC GGGTGCAAGG ACAGGAGCAG CAGACACAGG ATCCGAAGTC TTCCTGCAGC      720
CAT                                                                    723

```

(2) INFORMATION FOR SEQ ID NO:179:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 471 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:179:

```

ATGGCTGCAG GAAGACTTCG GATCCTGTGT CTGCTGCTCC TGTCCTTGCA CCCGAGCCTC      60
GGCTGGGTCC TTGATCTTCA AGAGGCTTCT GTGGCAGATA AGCTCTCATT TGGGAAGATG      120
GCAGAGACTA GAGGGACCTG GACGCCCCAT CAGGGTAACA ACCATGTCCG TCTTCCAAGA      180
GCCTTGGCTG GTTCATGCCG ACTGTGGAGC CTGACCCTAC CAGTGGCTGA GCTGGGCCTG      240
GGCTATGCCT CGGAGGAGAA GGTCATCTTC CGATACTGTG CTGGCAGCTG TCCCCAAGAG      300
GCCCCGTACCC AGCACAGTCT GGTACTGGCC CGGCTTCGAG GCGGGGGTCG AGCCCATGGC      360
CGACCCTGCT GCCAGCCCAC CAGCTATGCT GATGTGACCT TCCTTGATGA TCAGCACCAT      420
TGGCAGCAGC TGCCTCAGCT CTCAGCTGCA GCTTGTGGCT GTGGTGGCTG A              471

```

(2) INFORMATION FOR SEQ ID NO:180:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 471 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:180:

```

TCAGCCACCA CAGCCACAAG CTGCAGCTGA GAGCTGAGGC AGCTGCTGCC AATGGTGCTG      60
ATCATCAAGG AAGGTCACAT CAGCATAGCT GGTGGGCTGG CAGCAGGGTC GGCCATGGGC      120
TCGACCCCGC CCTCGAAGCC GGGCCAGTAC CAGACTGTGC TGGGTACGGG CCTCTTGGGG      180
ACAGCTGCCA GCACAGTATC GGAAGATGAC CTTCTCCTCC GAGGCATAGC CCAGGCCCAG      240
CTCAGCCACT GGTAGGGTCA GGCTCCACAG TCGGCATGAA CCAGCCAAGG CTCTTGGAAG      300
ACGGACATGG TTGTTACCCT GATGGGGCGT CCAGGTCCCT CTAGTCTCTG CCATCTTCCC      360
AAATGAGAGC TTATCTGCCA CAGAAGCCTC TTGAAGATCA AGGACCCAGC CGAGGCTCGG      420
GTGCAAGGAC AGGAGCAGCA GACACAGGAT CCGAAGTCTT CCTGCAGCCA T              471

```

(2) INFORMATION FOR SEQ ID NO:181:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 180 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:181:

```

ATGGCTGCAG GAAGACTTCG GATCCTGTGT CTGCTGCTCC TGTCCTTGCA CCCGAGCCTC      60
GGCTGGGTCC TTGATCTTCA AGAGGCTTCT GTGGCAGATA AGCTCTCATT TGGGAAGATG      120
GCAGAGACTA GAGGGACCTG GACGCCCCAT CAGGGTAACA ACCATGTCCG TCTTCCAAGA      180

```

(2) INFORMATION FOR SEQ ID NO:182:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 180 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:182:

```

TCTTGGAAGA CGGACATGGT TGTTACCCTG ATGGGGCGTC CAGGTCCCTC TAGTCTCTGC      60
CATCTTCCCA AATGAGAGCT TATCTGCCAC AGAAGCCTCT TGAAGATCAA GGACCCAGCC      120
GAGGCTCGGG TGCAAGGACA GGAGCAGCAG ACACAGGATC CGAAGTCTTC CTGCAGCCAT      180

```

(2) INFORMATION FOR SEQ ID NO:183:

- (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 291 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:183:

```
GCCTTGGCTG GTTCATGCCG ACTGTGGAGC CTGACCCTAC CAGTGGCTGA GCTGGGCCTG      60
GGCTATGCCT CGGAGGAGAA GGTCACTCTC CGATACTGTG CTGGCAGCTG TCCCCAAGAG      120
GCCCCGTACCC AGCACAGTCT GGTACTGGCC CGGCTTCGAG GCGGGGGTCG AGCCCATGGC      180
CGACCCTGCT GCCAGCCCAC CAGCTATGCT GATGTGACCT TCCTTGATGA TCAGCACCAT      240
TGGCAGCAGC TGCCTCAGCT CTCAGCTGCA GCTTGTGGCT GTGGTGGCTG A                291
```

(2) INFORMATION FOR SEQ ID NO:184:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 291 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:184:

```
TCAGCCACCA CAGCCACAAG CTGCAGCTGA GAGCTGAGGC AGCTGCTGCC AATGGTGCTG      60
ATCATCAAGG AAGGTCACAT CAGCATAGCT GGTGGGCTGG CAGCAGGGTC GGCCATGGGC      120
TCGACCCCGC CCTCGAAGCC GGGCCAGTAC CAGACTGTGC TGGGTACGGG CCTCTTGGGG      180
ACAGCTGCCA GCACAGTATC GGAAGATGAC CTTCTCCTCC GAGGCATAGC CCAGGCCCCAG      240
CTCAGCCACT GGTAGGGTCA GGCTCCACAG TCGGCATGAA CCAGCCAAGG C                291
```

(2) INFORMATION FOR SEQ ID NO:185:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 156 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:185:

```
Met Ala Ala Gly Arg Leu Arg Ile Leu Cys Leu Leu Leu Ser Leu
1           5           10           15
```

```
His Pro Ser Leu Gly Trp Val Leu Asp Leu Gln Glu Ala Ser Val Ala
```

| | | |
|---|-----|-----|
| 20 | 25 | 30 |
| Asp Lys Leu Ser Phe Gly Lys Met Ala Glu Thr Arg Gly Thr Trp Thr | | |
| 35 | 40 | 45 |
| Pro His Gln Gly Asn Asn His Val Arg Leu Pro Arg Ala Leu Ala Gly | | |
| 50 | 55 | 60 |
| Ser Cys Arg Leu Trp Ser Leu Thr Leu Pro Val Ala Glu Leu Gly Leu | | |
| 65 | 70 | 75 |
| Gly Tyr Ala Ser Glu Gly Lys Val Ile Phe Arg Tyr Cys Ala Gly Ser | | |
| 85 | 90 | 95 |
| Cys Pro Gln Glu Ala Arg Thr Gln His Ser Leu Val Leu Ala Arg Leu | | |
| 100 | 105 | 110 |
| Arg Gly Arg Gly Arg Ala His Gly Arg Pro Cys Cys Gln Pro Thr Ser | | |
| 115 | 120 | 125 |
| Tyr Ala Asp Val Thr Phe Leu Asp Asp Gln His His Trp Gln Gln Leu | | |
| 130 | 135 | 140 |
| Pro Gln Leu Ser Ala Ala Ala Cys Gly Cys Gly Gly | | |
| 145 | 150 | 155 |

(2) INFORMATION FOR SEQ ID NO:186:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 60 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:186:

| | | |
|---|----|----|
| Met Ala Ala Gly Arg Leu Arg Ile Leu Cys Leu Leu Leu Ser Leu | | |
| 1 | 5 | 10 |
| His Pro Ser Leu Gly Trp Val Leu Asp Leu Gln Glu Ala Ser Val Ala | | |
| 20 | 25 | 30 |
| Asp Lys Leu Ser Phe Gly Lys Met Ala Glu Thr Arg Gly Thr Trp Thr | | |
| 35 | 40 | 45 |
| Pro His Gln Gly Asn Asn His Val Arg Leu Pro Arg | | |
| 50 | 55 | 60 |

(2) INFORMATION FOR SEQ ID NO:187:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 96 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:187:

Ala Leu Ala Gly Ser Cys Arg Leu Trp Ser Leu Thr Leu Pro Val Ala
 1 5 10 15
 Glu Leu Gly Leu Gly Tyr Ala Ser Glu Glu Lys Val Ile Phe Arg Tyr
 20 25 30
 Cys Ala Gly Ser Cys Pro Gln Glu Ala Arg Thr Gln His Ser Leu Val
 35 40 45
 Leu Ala Arg Leu Arg Gly Arg Gly Arg Ala His Gly Arg Pro Cys Cys
 50 55 60
 Gln Pro Thr Ser Tyr Ala Asp Val Thr Phe Leu Asp Asp Gln His His
 65 70 75 80
 Trp Gln Gln Leu Pro Gln Leu Ser Ala Ala Ala Cys Gly Cys Gly Gly
 85 90 95

(2) INFORMATION FOR SEQ ID NO:188:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 559 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:188:

ATGGCTGCAG GAAGACTTCG GATCTTGTTT CTGCTGCTCC TGTCCTTGCA CCTGGGCCTT 60
 GGCTGGGTCC TTGATCTTCA AGAGGCTCCT GCGGCAGATG AGCTCTCATC TGGGAAAATG 120
 GCAGAGACTG GAAGGACCTG GAAGCCCCAT CAGGGTAAGA ATTCTTGGGG GCCTCCTAAC 180
 TCTACAGTTC TTCCTCTCAA AGCCCTCACT TTGCCTCACA ATCCTATTCT ACCTTGCACT 240
 AGGTAACAAC AATGTCCGCC TTCCAAGAGC CTTACCTGGT TTGTGCCGGC TGTGGAGCCT 300
 GACCCACCA GTGGCTGAGC TTGGCCTGGG CTATGCCTCA GAGGAGAAGA TTATCTTCCG 360
 ATACTGTGCT GGCAGCTGTC CCCAAGAGGT CCGTACCCAG CACAGTCTGG TGCTGGCCCCG 420
 TCTTCGAGGG CAGGGTCGAG CTCATGGCAG ACCTTGCTGC CAGCCCACCA GCTATGCTGA 480
 TGTGACCTTC CTTGATGACC ACCACCATG GCAGCAGCTG CCTCAGCTCT CAGCCGCAGC 540
 TTGTGGCTGT GGTGGCTGA 559

(2) INFORMATION FOR SEQ ID NO:189:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 559 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:189:

| | |
|--|-----|
| TCAGCCACCA CAGCCACAAG CTGCGGCTGA GAGCTGAGGC AGCTGCTGCC AATGGTGGTG | 60 |
| GTCATCAAGG AAGGTCACAT CAGCATAGCT GGTGGGCTGG CAGCAAGGTC TGCCATGAGC | 120 |
| TCGACCCTGC CCTCGAAGAC GGGCCAGCAC CAGACTGTGC TGGGTACGGA CCTCTTGGGG | 180 |
| ACAGCTGCCA GCACAGTATC GGAAGATAAT CTTCTCCTCT GAGGCATAGC CCAGGCCAAG | 240 |
| CTCAGCCACT GGTAGGGTCA GGCTCCACAG CCGGCACAAA CCAGGTAAGG CTCTTGGAAG | 300 |
| GCGGACATTG TTGTTACCTA GTGCAAGGTA GAATAGGATT GTGAGGCAAA GTGAGGGCTT | 360 |
| TGAGAGGAAG AACTGTAGAG TTAGGAGGCC CCCAAGAATT CTTACCCTGA TGGGGCTTCC | 420 |
| AGGTCCTTCC AGTCTCTGCC ATTTTCCAG ATGAGAGCTC ATCTGCCGCA GGAGCCTCTT | 480 |
| GAAGATCAAG GACCCAGCCA AGGCCCAGGT GCAAGGACAG GAGCAGCAGA AACAAAGATCC | 540 |
| GAAGTCTTCC TGCAGCCAT | 559 |

(2) INFORMATION FOR SEQ ID NO:190:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 471 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:190:

| | |
|---|-----|
| ATGGCTGCAG GAAGACTTCG GATCTTGTTT CTGCTGCTCC TGTCCTTGCA CCTGGGCCTT | 60 |
| GGCTGGGTCC TTGATCTTCA AGAGGCTCCT GCGGCAGATG AGCTCTCATC TGGGAAAATG | 120 |
| GCAGAGACTG GAAGGACCTG GAAGCCCCAT CAGGGTAACA ACAATGTCCG CCTTCCAAGA | 180 |
| GCCTTACCTG GTTTGTGCCG GCTGTGGAGC CTGACCCTAC CAGTGGCTGA GCTTGGCCTG | 240 |
| GGCTATGCCT CAGAGGAGAA GATTATCTTC CGATACTGTG CTGGCAGCTG TCCCCAAGAG | 300 |
| GTCCGTACCC AGCACAGTCT GGTGCTGGCC CGTCTTCGAG GGCAGGGTCG AGCTCATGGC | 360 |
| AGACCTTGCT GCCAGCCAC CAGCTATGCT GATGTGACCT TCCTTGATGA CCACCACCAT | 420 |
| TGGCAGCAGC TGCCTCAGCT CTCAGCCGCA GCTTGTGGCT GTGGTGGCTG A | 471 |

(2) INFORMATION FOR SEQ ID NO:191:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 471 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:191:

| | |
|---|-----|
| TCAGCCACCA CAGCCACAAG CTGCGGCTGA GAGCTGAGGC AGCTGCTGCC AATGGTGGTG | 60 |
| GTCATCAAGG AAGGTCACAT CAGCATAGCT GGTGGGCTGG CAGCAAGGTC TGCCATGAGC | 120 |
| TCGACCCTGC CCTCGAAGAC GGGCCAGCAC CAGACTGTGC TGGGTACGGA CCTCTTGGGG | 180 |
| ACAGCTGCCA GCACAGTATC GGAAGATAAT CTTCTCCTCT GAGGCATAGC CCAGGCCAAG | 240 |
| CTCAGCCACT GGTAGGTCA GGCTCCACAG CCGGCACAAA CCAGGTAAGG CTCTTGAAG | 300 |
| GCGGACATTG TTGTTACCCT GATGGGGCTT CCAGGTCCTT CCAGTCTCTG CCATTTTCCC | 360 |
| AGATGAGAGC TCATCTGCCG CAGGAGCCTC TTGAAGATCA AGGACCCAGC CAAGGCCAG | 420 |
| GTGCAAGGAC AGGAGCAGCA GAAACAAGAT CCGAAGTCTT CCTGCAGCCA T | 471 |

(2) INFORMATION FOR SEQ ID NO:192:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 180 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:192:

| | |
|---|-----|
| ATGGCTGCAG GAAGACTTCG GATCTTGTTT CTGCTGCTCC TGTCTTGCA CCTGGGCCTT | 60 |
| GGCTGGGTCC TTGATCTTCA AGAGGCTCCT GCGGCAGATG AGCTCTCATC TGGGAAAATG | 120 |
| GCAGAGACTG GAAGGACCTG GAAGCCCCAT CAGGGTAACA ACAATGTCCG CCTTCCAAGA | 180 |

(2) INFORMATION FOR SEQ ID NO:193:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 180 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:193:

| | |
|---|-----|
| TCTTGGAAGG CGGACATTGT TGTTACCCTG ATGGGGCTTC CAGGTCCTTC CAGTCTCTGC | 60 |
| CATTTTCCCA GATGAGAGCT CATCTGCCGC AGGAGCCTCT TGAAGATCAA GGACCCAGCC | 120 |
| AAGGCCCAGG TGCAAGGACA GGAGCAGCAG AAACAAGATC CGAAGTCTTC CTGCAGCCAT | 180 |

(2) INFORMATION FOR SEQ ID NO:194:

- (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 291 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:194:

```
GCCTTACCTG GTTTGTGCCG GCTGTGGAGC CTGACCCTAC CAGTGGCTGA GCTTGGCCTG      60
GGCTATGCCT CAGAGGAGAA GATTATCTTC CGATACTGTG CTGGCAGCTG TCCCCAAGAG      120
GTCCGTACCC AGCACAGTCT GGTGCTGGCC CGTCTTCGAG GGCAGGGTCG AGCTCATGGC      180
AGACCTTGCT GCCAGCCCAC CAGCTATGCT GATGTGACCT TCCTTGATGA CCACCACCAT      240
TGGCAGCAGC TGCCTCAGCT CTCAGCCGCA GCTTGTGGCT GTGGTGGCTG A                291
```

(2) INFORMATION FOR SEQ ID NO:195:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 291 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:195:

```
TCAGCCACCA CAGCCACAAG CTGCGGCTGA GAGCTGAGGC AGCTGCTGCC AATGGTGGTG      60
GTCATCAAGG AAGGTCACAT CAGCATAGCT GGTGGGCTGG CAGCAAGGTC TGCCATGAGC      120
TCGACCCTGC CCTCGAAGAC GGGCCAGCAC CAGACTGTGC TGGGTACGGA CCTCTTGGGG      180
ACAGCTGCCA GCACAGTATC GGAAGATAAT CTTCTCCTCT GAGGCATAGC CCAGGCCAAG      240
CTCAGCCACT GGTAGGGTCA GGCTCCACAG CCGGCACAAA CCAGGTAAGG C                291
```

(2) INFORMATION FOR SEQ ID NO:196:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 156 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:196:

```
Met Ala Ala Gly Arg Leu Arg Ile Leu Phe Leu Leu Leu Leu Ser Leu
 1           5           10           15
```


His Leu Gly Leu Gly Trp Val Leu Asp Leu Gln Glu Ala Pro Ala Ala
 20 25 30
 Asp Glu Leu Ser Ser Gly Lys Met Ala Glu Thr Gly Arg Thr Trp Lys
 35 40 45
 Pro His Gln Gly Asn Asn Asn Val Arg Leu Pro Arg Ala Leu Pro Gly
 50 55 60
 Leu Cys Arg Leu Trp Ser Leu Thr Leu Pro Val Ala Glu Leu Gly Leu
 65 70 75 80
 Gly Tyr Ala Ser Glu Glu Lys Ile Ile Phe Arg Tyr Cys Ala Gly Ser
 85 90 95
 Cys Pro Gln Glu Val Arg Thr Gln His Ser Leu Val Leu Ala Arg Leu
 100 105 110
 Arg Gly Gln Gly Arg Ala His Gly Arg Pro Cys Cys Gln Pro Thr Ser
 115 120 125
 Tyr Ala Asp Val Thr Phe Leu Asp Asp His His His Trp Gln Gln Leu
 130 135 140
 Pro Gln Leu Ser Ala Ala Ala Cys Gly Cys Gly Gly
 145 150 155

(2) INFORMATION FOR SEQ ID NO:197:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 60 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:197:

Met Ala Ala Gly Arg Leu Arg Ile Leu Phe Leu Leu Leu Leu Ser Leu
 1 5 10 15
 His Leu Gly Leu Gly Trp Val Leu Asp Leu Gln Glu Ala Pro Ala Ala
 20 25 30
 Asp Glu Leu Ser Ser Gly Lys Met Ala Glu Thr Gly Arg Thr Trp Lys
 35 40 45
 Pro His Gln Gly Asn Asn Asn Val Arg Leu Pro Arg
 50 55 60

(2) INFORMATION FOR SEQ ID NO:198:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 96 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:198:

Ala Leu Pro Gly Leu Cys Arg Leu Trp Ser Leu Thr Leu Pro Val Ala
 1 5 10 15
 Glu Leu Gly Leu Gly Tyr Ala Ser Glu Glu Lys Ile Ile Phe Arg Tyr
 20 25 30
 Cys Ala Gly Ser Cys Pro Gln Glu Val Arg Thr Gln His Ser Leu Val
 35 40 45
 Leu Ala Arg Leu Arg Gly Gln Gly Arg Ala His Gly Arg Pro Cys Cys
 50 55 60
 Gln Pro Thr Ser Tyr Ala Asp Val Thr Phe Leu Asp Asp His His His
 65 70 75 80
 Trp Gln Gln Leu Pro Gln Leu Ser Ala Ala Ala Cys Gly Cys Gly Gly
 85 90 95

(2) INFORMATION FOR SEQ ID NO:199:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 291 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:199:

GCCCTGTCTG GTCCATGCCA GCTGTGGAGC CTGACCCTGT CCGTGGCAGA GCTAGGCCTG 60
 GGCTACGCCT CAGAGGAGAA GGTCACTTTC CGTACTGCG CCGGCAGCTG CCCCCGTGGT 120
 GCCCGCACCC AGCATGGCCT GGCGCTGGCC CGGCTGCAGG GCCAGGGCCG AGCCCACGGT 180
 GGGCCCTGCT GCCGGCCAC TCGCTACACC GACGTGGCCT TCCTCGATGA CCGCCACCGC 240
 TGGCAGCGGC TGCCCCAGCT CTCGGCGGCT GCCTGCGGCT GTGGTGGCTG A 291

(2) INFORMATION FOR SEQ ID NO:200:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 291 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:200:

TCAGCCACCA CAGCCGAGG CAGCCGCCGA GAGCTGGGGC AGCCGCTGCC AGCGGTGGCG 60
 GTCATCGAGG AAGGCCACGT CGGTGTAGCG AGTGGGCCGG CAGCAGGGCC CACCGTGGGC 120

TCGGCCCTGG CCCTGCAGCC GGGCCAGCGC CAGGCCATGC TGGGTGCGGG CACCACGGGG 180
 GCAGCTGCCG GCGCAGTAGC GGAAGATGAC CTTCTCCTCT GAGGCGTAGC CCAGGCCTAG 240
 CTCTGCCACG GACAGGGTCA GGCTCCACAG CTGGCATGGA CCAGACAGGG C 291

(2) INFORMATION FOR SEQ ID NO:201:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 291 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:201:

GCCCTGTCTG GTCCATGCCA GCTGTGGAGC CTGACCCTGT CCGTGGCAGA GCTAGGCCTG 60
 GGCTACGCCT CAGAGGAGAA GGTCATCTTC CGCTACTGCG CCGGCAGCTG CCCCCGTGGT 120
 GCGCGACCC AGCATGGCCT GCGCTGGCC CGGCTGCAGG GCCAGGGCCG AGCCCACGGC 180
 GGGCCCTGCT GCGGCCCCAC TCGCTACACC GACGTGGCCT TCCTCGATGA CCGCCACCGC 240
 TGGCAGCGGC TGCCCCAGCT CTCGGCGGCT GCCTGCGGCT GTGGTGGCTG A 291

(2) INFORMATION FOR SEQ ID NO:202:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 291 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:202:

TCAGCCACCA CAGCCGCAGG CAGCCGCCGA GAGCTGGGGC AGCCGCTGCC AGCGGTGGCG 60
 GTCATCGAGG AAGGCCACGT CCGTGTAGCG AGTGGGCCGG CAGCAGGGCC CGCCGTGGGC 120
 TCGGCCCTGG CCCTGCAGCC GGGCCAGCGC CAGGCCATGC TGGGTGCGGG CACCACGGGG 180
 GCAGCTGCCG GCGCAGTAGC GGAAGATGAC CTTCTCCTCT GAGGCGTAGC CCAGGCCTAG 240
 CTCTGCCACG GACAGGGTCA GGCTCCACAG CTGGCATGGA CCAGACAGGG C 291

(2) INFORMATION FOR SEQ ID NO:203:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 471 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:203:

```

ATGGCCGTAG GGAAGTTCCT GCTGGGCTCT CTGCTGCTCC TGTCCCTGCA GCTGGGACAG      60
GGCTGGGGCC CCGATGCCCC TGGGGTTCCC GTGGCCGATG GAGAGTTCTC GTCTGAACAG      120
GTGGCAAAGG CTGGAGGGAC CTGGCTGGGC ACCCACC GCCCCTTGCCCG CCTGCGCCGA      180
GCCCTGTCTG GTCCATGCCA GCTGTGGAGC CTGACCCTGT CCGTGGCAGA GCTAGGCCTG      240
GGCTACGCCT CAGAGGAGAA GGTCACTTTC CGCTACTGCG CCGGCAGCTG CCCCCGTGGT      300
GCCCGCACCC AGCATGGCCT GGCCTGGCC CGGCTGCAGG GCCAGGGCCG AGCCCACGGT      360
GGGCCCTGCT GCCGGCCAC TCGCTACACC GACGTGGCCT TCCTCGATGA CCGCCACCGC      420
TGGCAGCGGC TGCCCCAGCT CTCGGCGGCT GCCTGCGGCT GTGGTGGCTG A              471

```

(2) INFORMATION FOR SEQ ID NO:204:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 471 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:204:

```

TCAGCCACCA CAGCCGCAGG CAGCCGCCGA GAGCTGGGGC AGCCGCTGCC AGCGGTGGCG      60
GTCATCGAGG AAGGCCACGT CGGTGTAGCG AGTGGGCCGG CAGCAGGGCC CACCGTGGGC      120
TCGGCCCTGG CCCTGCAGCC GGGCCAGCGC CAGGCCATGC TGGGTGCGGG CACCACGGGG      180
GCAGCTGCCG GCGCAGTAGC GGAAGATGAC CTTCTCCTCT GAGGCGTAGC CCAGGCCTAG      240
CTCTGCCACG GACAGGTCA GGCTCCACAG CTGGCATGGA CCAGACAGGG CTCGCGCGAG      300
GCGGGCAAGG GGGCGGTGGG TGCCCAGCCA GGTCCCTCCA GCCTTTGCCA CCTGTTCAGA      360
CGAGAACTCT CCATCGGCCA CGGGAACCCC ACGGGCATCG GGGCCCCAGC CCTGTCCCAG      420
CTGCAGGGAC AGGAGCAGCA GAGAGCCCAG CAGGAACTTC CCTACGGCCA T              471

```

(2) INFORMATION FOR SEQ ID NO:205:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 471 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:205:

```

ATGGCCGTAG GGAAGTTCCT GCTGGGCTCC CTGCTGCTCC TGTCCCTGCA GCTGGGACAG      60
GGCTGGGGCC CCGATGCCCC TGGGGTTCCC GTGGCCGATG GAGAGTTCTC GTCTGAACAG      120
GTGGCAAAGG CTGGAGGGAC CTGGCTGGGC ACCCACC GCCC CCCTTGCCCC CCGCGCCGA      180
GCCCTGTCTG GTCCATGCCA GCTGTGGAGC CTGACCCTGT CCGTGGCAGA GCTAGGCCTG      240
GGCTACGCCT CAGAGGAGAA GGTCACTCTC CGCTACTGCG CCGGCAGCTG CCCCCGTGGT      300
GGCCGCACCC AGCATGGCCT GGCCTGGCC CGGCTGCAGG GCCAGGGCCG AGCCCACGGC      360
GGGCCCTGCT GCGGCCCCAC TCGCTACACC GACGTGGCCT TCCTCGATGA CCGCCACCGC      420
TGGCAGCGGC TGCCCCAGCT CTCGGCGGCT GCCTGCGGCT GTGGTGGCTG A              471

```

(2) INFORMATION FOR SEQ ID NO:206:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 471 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:206:

```

TCAGCCACCA CAGCCGCAGG CAGCCGCCGA GAGCTGGGGC AGCCGCTGCC AGCGGTGGCG      60
GTCATCGAGG AAGGCCACGT CGGTGTAGCG AGTGGGCCGG CAGCAGGGCC CGCCGTGGGC      120
TCGGCCCTGG CCCTGCAGCC GGGCCAGCGC CAGGCCATGC TGGGTGCGGG CACCACGGGG      180
GCAGCTGCCG GCGCAGTAGC GGAAGATGAC CTTCTCCTCT GAGGCGTAGC CCAGGCCTAG      240
CTCTGCCACG GACAGGGTCA GGCTCCACAG CTGGCATGGA CCAGACAGGG CTCGGCGCAG      300
GCGGGCAAGG GGGCGGTGGG TGCCCAGCCA GGTCCCTCCA GCCTTTGCCA CCTGTTCAGA      360
CGAGAACTCT CCATCGGCCA CGGGAACCCC ACGGGCATCG GGGCCCCAGC CCTGTCCAG      420
CTGCAGGGAC AGGAGCAGCA GGGAGCCCAG CAGGAACTTC CCTACGGCCA T              471

```

(2) INFORMATION FOR SEQ ID NO:207:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 69 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:207:

```

ATGGCCGTAG GGAAGTTCCT GCTGGGCTCT CTGCTGCTCC TGTCCCTGCA GCTGGGACAG      60
GGCTGGGGC                                     69

```

(2) INFORMATION FOR SEQ ID NO:208:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 69 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:208:

GCCCCAGCCC TGTCCCAGCT GCAGGGACAG GAGCAGCAGA GAGCCCAGCA GGAAGTTCCC 60
TACGGCCAT 69

(2) INFORMATION FOR SEQ ID NO:209:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 69 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:209:

ATGGCCGTAG GGAAGTTCCT GCTGGGCTCC CTGCTGCTCC TGTCCCTGCA GCTGGGACAG 60
GGCTGGGGC 69

(2) INFORMATION FOR SEQ ID NO:210:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 69 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:210:

GCCCCAGCCC TGTCCCAGCT GCAGGGACAG GAGCAGCAGG GAGCCCAGCA GGAAGTTCCC 60
TACGGCCAT 69

(2) INFORMATION FOR SEQ ID NO:211:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 111 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:211:

```
CCCGATGCCC GTGGGGTTCC CGTGGCCGAT GGAGAGTTCT CGTCTGAACA GGTGGCAAAG      60
GCTGGAGGGA CCTGGCTGGG CACCCACCGC CCCCTTGCCC GCCTGCGCCG A              111
```

(2) INFORMATION FOR SEQ ID NO:212:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 111 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:212:

```
TCGGCGCAGG CGGGCAAGGG GCGGTGGGT GCCAGCCAG GTCCCTCCAG CCTTTGCCAC      60
CTGTTCAGAC GAGAACTCTC CATCGGCCAC GGAACCCCA CGGGCATCGG G              111
```

(2) INFORMATION FOR SEQ ID NO:213:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 180 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:213:

```
ATGGCCGTAG GGAAGTTCCT GCTGGGCTCT CTGCTGCTCC TGTCCCTGCA GCTGGGACAG      60
GGCTGGGGCC CCGATGCCCC TGGGGTTCCC GTGGCCGATG GAGAGTTCTC GTCTGAACAG      120
GTGGCAAAGG CTGGAGGGAC CTGGCTGGGC ACCCACC GCCC CCCTTGCCCC CCTGCGCCGA      180
```

(2) INFORMATION FOR SEQ ID NO:214:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 180 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:214:

TCGGCGCAGG CGGGCAAGGG GGCGGTGGGT GCCCAGCCAG GTCCCTCCAG CCTTTGCCAC 60
 CTGTTTCAGAC GAGAACTCTC CATCGGCCAC GGAACCCCA CGGGCATCGG GGCCCCAGCC 120
 CTGTCCCAGC TGCAGGGACA GGAGCAGCAG AGAGCCCAGC AGGAACTTCC CTACGGCCAT 180

(2) INFORMATION FOR SEQ ID NO:215:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 180 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:215:

ATGGCCGTAG GGAAGTTCCT GCTGGGCTCC CTGCTGCTCC TGTCCTGCA GCTGGGACAG 60
 GGCTGGGGCC CCGATGCCCCG TGGGGTTCCT GTGGCCGATG GAGAGTTCTC GTCTGAACAG 120
 GTGGCAAAGG CTGGAGGGAC CTGGCTGGGC ACCCACC GCCCCTTGCCCC CCTGCGCCGA 180

(2) INFORMATION FOR SEQ ID NO:216:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 180 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:216:

TCGGCGCAGG CGGGCAAGGG GGCGGTGGGT GCCCAGCCAG GTCCCTCCAG CCTTTGCCAC 60
 CTGTTTCAGAC GAGAACTCTC CATCGGCCAC GGAACCCCA CGGGCATCGG GGCCCCAGCC 120
 CTGTCCCAGC TGCAGGGACA GGAGCAGCAG GGAGCCCAGC AGGAACTTCC CTACGGCCAT 180

(2) INFORMATION FOR SEQ ID NO:217:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 156 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:217:

Met Ala Val Gly Lys Phe Leu Leu Gly Ser Leu Leu Leu Ser Leu
 1 5 10 15

Gln Leu Gly Gln Gly Trp Gly Pro Asp Ala Arg Gly Val Pro Val Ala
 20 25 30
 Asp Gly Glu Phe Ser Ser Glu Gln Val Ala Lys Ala Gly Gly Thr Trp
 35 40 45
 Leu Gly Thr His Arg Pro Leu Ala Arg Leu Arg Arg Ala Leu Ser Gly
 50 55 60
 Pro Cys Gln Leu Trp Ser Leu Thr Leu Ser Val Ala Glu Leu Gly Leu
 65 70 75 80
 Gly Tyr Ala Ser Glu Glu Lys Val Ile Phe Arg Tyr Cys Ala Gly Ser
 85 90 95
 Cys Pro Arg Gly Ala Arg Thr Gln His Gly Leu Ala Leu Ala Arg Leu
 100 105 110
 Gln Gly Gln Gly Arg Ala His Gly Gly Pro Cys Cys Arg Pro Thr Arg
 115 120 125
 Tyr Thr Asp Val Ala Phe Leu Asp Asp Arg His Arg Trp Gln Arg Leu
 130 135 140
 Pro Gln Leu Ser Ala Ala Ala Cys Gly Cys Gly Gly
 145 150 155

(2) INFORMATION FOR SEQ ID NO:218:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 60 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:218:

Met Ala Val Gly Lys Phe Leu Leu Gly Ser Leu Leu Leu Leu Ser Leu
 1 5 10 15
 Gln Leu Gly Gln Gly Trp Gly Pro Asp Ala Arg Gly Val Pro Val Ala
 20 25 30
 Asp Gly Glu Phe Ser Ser Glu Gln Val Ala Lys Ala Gly Gly Thr Trp
 35 40 45
 Leu Gly Thr His Arg Pro Leu Ala Arg Leu Arg Arg
 50 55 60

(2) INFORMATION FOR SEQ ID NO:219:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 23 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:219:

Met Ala Val Gly Lys Phe Leu Leu Gly Ser Leu Leu Leu Leu Ser Leu
 1 5 10 15
 Gln Leu Gly Gln Gly Trp Gly
 20

(2) INFORMATION FOR SEQ ID NO:220:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 37 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:220:

Pro Asp Ala Arg Gly Val Pro Val Ala Asp Gly Glu Phe Ser Ser Glu
 1 5 10 15
 Gln Val Ala Lys Ala Gly Gly Thr Trp Leu Gly Thr His Arg Pro Leu
 20 25 30
 Ala Arg Leu Arg Arg
 35

(2) INFORMATION FOR SEQ ID NO:221:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 96 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:221:

Ala Leu Ser Gly Pro Cys Gln Leu Trp Ser Leu Thr Leu Ser Val Ala
 1 5 10 15
 Glu Leu Gly Leu Gly Tyr Ala Ser Glu Glu Lys Val Ile Phe Arg Tyr
 20 25 30
 Cys Ala Gly Ser Cys Pro Arg Gly Ala Arg Thr Gln His Gly Leu Ala
 35 40 45
 Leu Ala Arg Leu Gln Gly Gln Gly Arg Ala His Gly Gly Pro Cys Cys
 50 55 60
 Arg Pro Thr Arg Tyr Thr Asp Val Ala Phe Leu Asp Asp Arg His Arg
 65 70 75 80
 Trp Gln Arg Leu Pro Gln Leu Ser Ala Ala Ala Cys Gly Cys Gly Gly
 85 90 95

(2) INFORMATION FOR SEQ ID NO:222:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 267 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:222:

```

TGCCAGCTGT GGAGCCTGAC CCTGTCCGTG GCAGAGCTAG GCCTGGGCTA CGCCTCAGAG      60
GAGAAGGTCA TCTTCCGCTA CTGCGCCGGC AGCTGCCCCC GTGGTGCCCG CACCCAGCAT      120
GGCCTGGCGC TGGCCCGGCT GCAGGGCCAG GGCCGAGCCC ACGGTGGGCC CTGCTGCCGG      180
CCCACTCGCT ACACCGACGT GGCCTTCCTC GATGACCGCC ACCGCTGGCA GCGGCTGCCC      240
CAGCTCTCGG CGGCTGCCTG CGGCTGT                                           267

```

(2) INFORMATION FOR SEQ ID NO:223:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 89 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:223:

```

Cys Gln Leu Trp Ser Leu Thr Leu Ser Val Ala Glu Leu Gly Leu Gly
1           5           10           15
Tyr Ala Ser Glu Glu Lys Val Ile Phe Arg Tyr Cys Ala Gly Ser Cys
20           25           30
Pro Arg Gly Ala Arg Thr Gln His Gly Leu Ala Leu Ala Arg Leu Gln
35           40           45
Gly Gln Gly Arg Ala His Gly Gly Pro Cys Cys Arg Pro Thr Arg Tyr
50           55           60
Thr Asp Val Ala Phe Leu Asp Asp Arg His Arg Trp Gln Arg Leu Pro
65           70           75           80
Gln Leu Ser Ala Ala Ala Cys Gly Cys
85

```

(2) INFORMATION FOR SEQ ID NO:224:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 5 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:224:

Ala Leu Ser Gly Pro
1 5

(2) INFORMATION FOR SEQ ID NO:225:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 24 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:225:

GTSASYGASY TGGGYCTGGG CTAY

24

(2) INFORMATION FOR SEQ ID NO:226:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 24 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:226:

TTYMGSTACT GCRSMGGCKC YTGC

24

(2) INFORMATION FOR SEQ ID NO:227:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 24 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:227:

RWAGGCSRTS G GKCKGCARC AKGS

24

(2) INFORMATION FOR SEQ ID NO:228:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 21 base pairs
(B) TYPE: nucleic acid

(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:228:

MKCRCTCYARR AASGACASST C

21

(2) INFORMATION FOR SEQ ID NO:229:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 168 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:229:

CGGCTTGTGA CCGAGCTGGG CCTGGGCTAC GCCTCAGAGG AGAAGGTCAT CTTCGGCTAC 60
TGCGCCGGCA GCTGCCCCCG TGGTGCCCGC ACCCAGCATG GCCTGGCGCT GGCCCGGCTG 120
CAGGGCCAGG GCCGAGCCCA CGGCGGGCCC TGCTGCCGCC CCATGGCC 168

(2) INFORMATION FOR SEQ ID NO:230:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:230:

GAGGAGAAGG TCATCTTCCG

20

(2) INFORMATION FOR SEQ ID NO:231:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:231:

GCCGTGGGCT CGGCCCTGGC

20

(2) INFORMATION FOR SEQ ID NO:232:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 24 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:232:

AGAGGAGAAG GTCATCTTCC GCTA

24

(2) INFORMATION FOR SEQ ID NO:233:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:233:

CTCGGCCCTG GCCCTGCAGC

20

(2) INFORMATION FOR SEQ ID NO:234:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:234:

TGCAGCCGGG CCAGCGCCAG

20

(2) INFORMATION FOR SEQ ID NO:235:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 31 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:235:

CGCGGATCCA TGCCTGGATT CGAGGGTGCA G

31

(2) INFORMATION FOR SEQ ID NO:236:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 31 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:236:

CGCGGATCCA TGGCCGTAGG GAAGTTCCTG C

31

(2) INFORMATION FOR SEQ ID NO:237:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 60 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:237:

CTCCCAAGCT TTTACTTGTC ATCGTCGTCC TTGTAGTCGC CACCACAGCC GCAGGCAGCC

60

(2) INFORMATION FOR SEQ ID NO:238:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 59 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:238:

CTCCCAAGCT TTTACTTGTC ATCGTCGTCC TTGTAGTCTC GAGGAAGGCC ACGTCGGTG

59

(2) INFORMATION FOR SEQ ID NO:239:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 25 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:239:

TCAGCCACCA CAGCCGCAGG CAGCC

25

(2) INFORMATION FOR SEQ ID NO:240:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 73 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:240:

| | | | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|--|--|
| Ser | Glu | Glu | Lys | Ile | Ile | Phe | Arg | Tyr | Cys | Ala | Gly | Ser | Cys | Pro | | | |
| | | | | 5 | | | | | 10 | | | | | 15 | | | |
| Gln | Glu | Val | Arg | Thr | Gln | His | Ser | Leu | Val | Leu | Ala | Arg | Leu | Arg | | | |
| | | | | 20 | | | | | 25 | | | | | 30 | | | |
| Gly | Gln | Gly | Arg | Ala | His | Gly | Arg | Pro | Cys | Cys | Gln | Pro | Thr | Ser | | | |
| | | | | 35 | | | | | 40 | | | | | 45 | | | |
| Tyr | Ala | Asp | Val | Thr | Phe | Leu | Asp | Asp | His | His | His | Trp | Gln | Gln | | | |
| | | | | 50 | | | | | 55 | | | | | 60 | | | |
| Leu | Pro | Gln | Leu | Ser | Ala | Ala | Ala | Cys | Gly | Cys | Gly | Gly | | | | | |
| | | | | 65 | | | | | 70 | | | | | | | | |

(2) INFORMATION FOR SEQ ID NO:241:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 93 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:241:

| | | | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|--|--|
| Cys | Val | Leu | Thr | Ala | Ile | His | Leu | Asn | Val | Thr | Asp | Leu | Gly | Leu | | | |
| | | | | 5 | | | | | 10 | | | | | 15 | | | |
| Gly | Tyr | Glu | Thr | Lys | Glu | Glu | Leu | Ile | Phe | Arg | Tyr | Cys | Ser | Gly | | | |
| | | | | 20 | | | | | 25 | | | | | 30 | | | |
| Ser | Cys | Glu | Ala | Ala | Glu | Thr | Met | Tyr | Asp | Lys | Ile | Leu | Lys | Asn | | | |
| | | | | 35 | | | | | 40 | | | | | 45 | | | |

Leu Ser Arg Ser Arg Arg Leu Thr Ser Asp Lys Val Gly Gln Ala
 50 55 60
 Cys Cys Arg Pro Val Ala Phe Asp Asp Asp Leu Ser Phe Leu Asp
 65 70 75
 Asp Ser Leu Val Tyr His Ile Leu Arg Lys His Ser Ala Lys Arg
 80 85 90
 Cys Gly Cys

(2) INFORMATION FOR SEQ ID NO:242:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 93 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:242:

Cys Val Leu Thr Ala Ile His Leu Asn Val Thr Asp Leu Gly Leu Gly
 5 10 15
 Tyr Glu Thr Lys Glu Glu Leu Ile Phe Arg Tyr Cys Ser Gly Ser Cys
 20 25 30
 Glu Ser Ala Glu Thr Met Tyr Asp Lys Ile Leu Lys Asn Leu Ser Arg
 35 40 45
 Ser Arg Arg Leu Thr Ser Asp Lys Val Gly Gln Ala Cys Cys Arg Pro
 50 55 60
 Val Ala Phe Asp Asp Asp Leu Ser Phe Leu Asp Asp Asn Leu Val Tyr
 65 70 75 80
 His Ile Leu Arg Lys His Ser Ala Lys Arg Cys Gly Cys
 85 90